Technical details of the IPHC MSE framework

CONTENTS

PURPOSE

To provide technical details of the International Pacific Halibut Commission (IPHC) Management Strategy Evaluation (MSE) framework.

1   INTRODUCTION

This technical document describes the Management Strategy Evaluation (MSE) framework and its elements, details specifications of the framework for the evaluation of scale and distribution management procedures, provides definition of terms used, and defines the technical details of the models and equations used within the framework. This is a working document that will be revised often as development of the MSE framework progresses. Therefore, this document is currently incomplete and will have occasional revisions.

1.1   Management Strategy Evaluation

MSE is a process to evaluate harvest strategies and develop a management procedure that is robust to uncertainty and meets defined objectives. It can be partitioned into four separate components that interact with each other (Figure 1). Management Procedures (MPs) are defined, often with input from stakeholders and managers but not necessarily, and evaluated against objectives which are determined with input from stakeholders and managers. Simulations of the various MPs are performed and evaluated against the objectives to identify the best performing MP to apply within a harvest strategy policy.
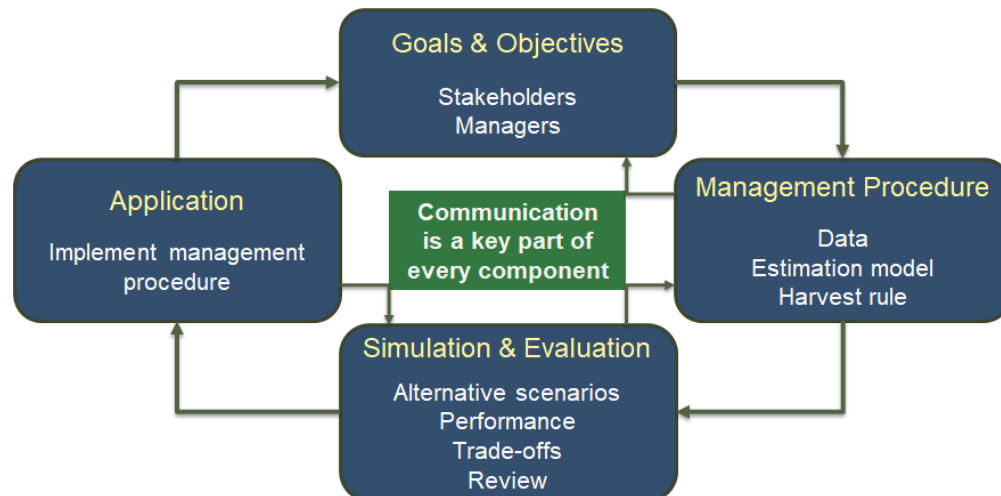
Figure 1: A depiction of the Management Strategy Evaluation (MSE) process showing the iterative nature of the process with the possibility of moving either direction between most components.

A harvest strategy policy can be implemented in a number of ways. Many fisheries are managed by applying the chosen management procedure each management cycle and implementing the results as management. Other agencies use the outcomes of the management procedure as a reference from which other considerations (e.g., socio-economic) are taken into account when determining a tactical decision of the management outcomes. This variability around the management procedure is called implementation variability and should be a part of the simulations and evaluation.

The four boxes shown in Figure 1 are all important component of an MSE. The objectives are the connection to stakeholders and managers. Performance metrics are derived from well-defined objectives that are used in the evaluation. Management procedures are the link to a transparent management process and need to be clearly defined so that they are formulaic and can be written as computer code for the closed-loop simulations. The closed-loop simulations also consist of an operating model which simulates the population and produces the observations needed for the management procedure. Applying the best performing MP is the goal of MSE but is not the end. The MSE should be updated as additional observations and knowledge is gained from the population, fishery, or management process.

The engine of the MSE process is the closed-loop simulation consisting of an operating model (OM) and a management procedure (MP, Figure 2).
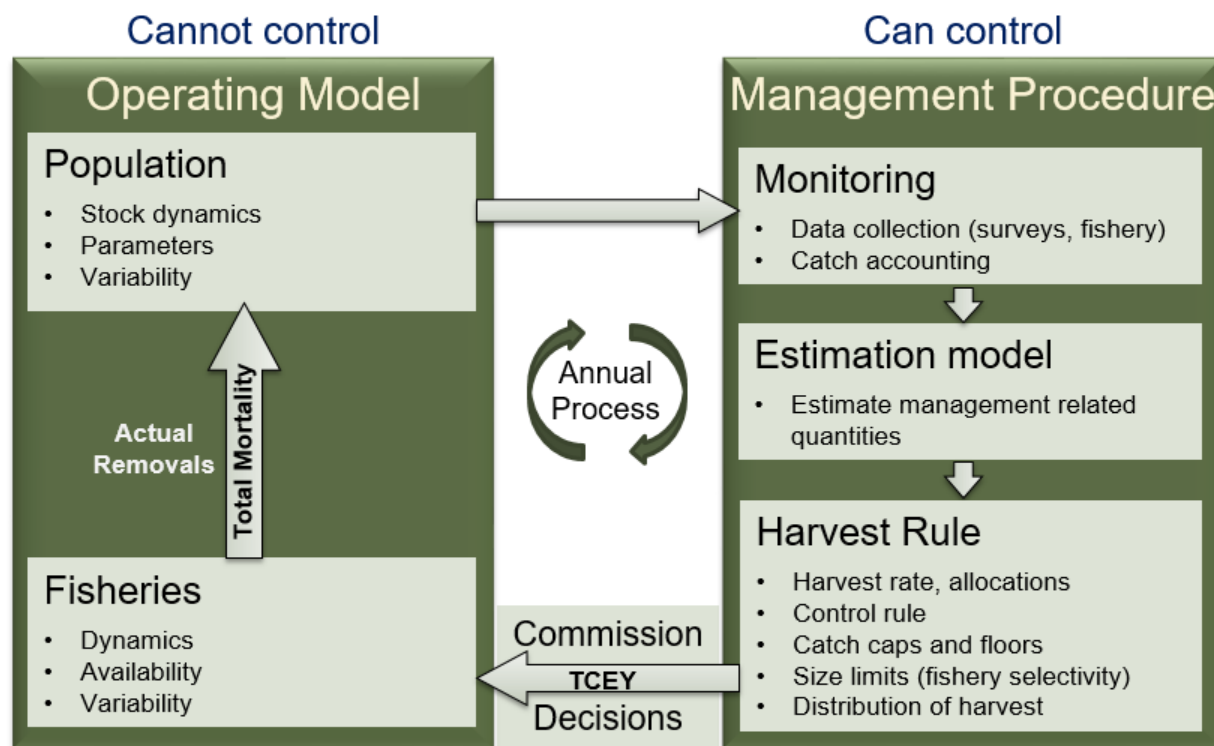
Figure 2: An illustration of the closed-loop simulation framework within the MSE process consisting of an operating model (OM) and a management procedure (MP).

The OM simulates the dynamics of the population and the fisheries that interact with it. The processes simulated by the OM can be thought of as processes that management does not, or chooses not, to control. For example, natural mortality is a process that is not directly managed, and some aspects of the fisheries are not managed (e.g. specific daily decisions). These unmanaged processes result in variability that is normal to the system, referred to as 'natural variability' in this document, and is simulated by the OM.

The MP consists of elements that are managed and may include data collection and monitoring, estimation models, and the harvest rules that determine how the fisheries are managed. MSE can evaluate any of these elements including how changes in monitoring, a different estimation model, or various harvest rules affect the outcomes. An element may be simple or complex.

The chapters in this document begin with this introduction describing MSE in general and an overview of the closed-loop simulation framework followed by the details of a generalized operating model that can be specified for any fish population. The specifications of the MSE for Pacific halibut fisheries are provided next following the three boxes in Figure 1 labeled Goals & Objectives, Management Procedure, and Simulation & Evaluation.

1.2   An overview of the closed-loop simulation framework

The closed-loop simulation framework includes elements that simulate the Pacific halibut population and fishery (Operating Model, OM) and management procedures (MPs) with a closed feedback loop (Figure 2). Each element of the framework is modular and can be modified independently. The OM is written in the programming language C++ with JavaScript Object Notation (JSON) input files and is flexible, fast, modular, and easily adapted to many different assumptions. The components of the framework that call the simulations and apply the MPs are coded in the R statistical language (R Core Team 2020). The files and executables necessary for a complete simulation are stored in three different folders.

- **Scenarios**: one folder contains the OM files and executable to run the projections (called 'Scenarios' here for convenience) along with outputs of the simulations. This is typically organized with a subfolder representing a specific scenario and folders within containing the OM file structure.

- **R**: another folder is called 'R' that contains all of the R scripts used to run the simulations. There are subfolders called MPs, RforAnalysis, RforEM, RfunctionsForMPs_static, and RunMPscripts.

- **EM**: a third folder called 'EM' contains the files and executable necessary to run the estimation model.

Each management procedure is simulated using one script that defines the number of simulations to run sequentially, sets the number of projection years, creates all the necessary folders to store output and results, and copies all necessary files over to the new folders. This script also calls the OM which begins by calculating the unfished equilibrium population given an input set of biological parameters. It then simulates the annual process during what is called an "initial period" which allows for the stock to distribute across modelled areas to an equilibrium state given recruitment deviations and initial fishing mortality (if desired). During a subsequent "main period", the population and dynamics are simulated using the input annual fishing mortality and time-varying parameters such as selectivity, recruitment variability, and annual movement between areas. The parameterized model that is run through to the end of the main period is called the conditioned model.

At the end of the main period the projection period begins. An R script containing all the details of the management procedure being evaluated as well as any other processes is called during the projection period. It projects weight-at-age as a random process (which may be done before starting the simulation if weight-at-age is not density-dependent). It generates data, with observation error, that are needed for estimation models (EMs) and MPs. It runs the estimation models of choice to provide an annual estimate of stock size and status and provides the coastwide mortality limits for the next time step as specified by the MP. It then applies the harvest control rule, to adjust the coastwide mortality limit accordingly, and distributes the coastwide mortality limit to IPHC Regulatory Areas. The final step is to allocate the mortality limits for each IPHC Regulatory Area to the different sectors within that area. These sector specific mortality limits are written to a JSON file (projectTMlim.json). Realized mortality, which may differ from the mortality limits, is written to 'projectTM.json'. These two files, along with 'projectWAA.json' containing simulated weight-at-age and 'projectSelRetDevs.json' containing selectivity and retention deviates are read back into the OM to simulate the fish population one year forward. This annual process (Figure 2) repeats a specified number of times. An unfished population with the exact same inputs other than fishing mortality is simulated in synchrony to the fished population for determination of a dynamic unfished population used in the calculation of dynamic reference points.

2 TECHNICAL DETAILS OF THE OPERATING MODEL

In a management strategy evaluation (MSE), operating models (OM) simulate the population and fishery dynamics. It incorporates life-history processes such as recruitment, growth, migration, maturation, and mortality of the fish population, as well as fishery processes such as selectivity, availability, and catchability. Descriptions of the various processes are provided below along with the mathematical equations used to simulate those processes. Many of the details are drawn from Hilborn and Walters (1992), Quinn and Deriso (1999), the CASAL manual (Bull, et al., 2012), Stock Synthesis technical details (Methot & Wetzel, 2013), and the Coleraine manual (Hilborn, et al., 2000).

There is uncertainty in the parameterization of the processes, natural variability in the processes, and multiple hypotheses about the mechanisms of the processes. These three sources of variability are introduced in three different ways.

Parameter uncertainty is introduced by conditioning the operating model to data and determining the distribution of uncertainty for each parameter as well as correlation with other parameters. Parameter values for an individual simulated trajectory are randomly drawn from the multivariate estimated probability distribution. Therefore, each simulated trajectory uses a different set of parameters, thus including variability that represents the uncertainty in the parameters.

Natural variability is introduced by defining a random process associated with various concepts. For example, recruitment varies naturally and is modelled by including random deviates applied annually to average recruitment. Other processes may have specific patterns such as changes in weight-at-age.

Structural uncertainty is included by defining multiple hypotheses and implementing them as separate operating models. For example, growth may occur in different ways between models. Or, data may be structured in a different way when conditioning the model. Structural uncertainty captures the variability that cannot be captured by the two methods above and may be integrated into the results or used to test unlikely but possible scenarios.

2.1 The state object

The state is the accounting of the population in numbers within an operating model and is contained in a state object with many dimensions. The state represents the intrinsic characteristics of the modeled population: age, maturity, and sex. This state is then evolved on a computational domain parameterized by time and space, which are defined as extrinsic variables. Furthermore, sectors (fisheries and survey) interact with the state. Clarified this way, the state object contains a representation of the stock at a place and time and can be subset along any of these axes as needed to determine the state for any combination of these dimensions.

The intrinsic and extrinsic dimensions are fixed inputs that are defined by the user, thus may be unique to any operating model. The different dimensions, and maximum ranges, are shown in Table 1. Maturity state (immature or mature) is not included as a dimension here but may be a useful characteristic to track for some stocks, depending on fishing intensity and the proportion maturing at age (possibly a further improvement). Instead, the mature population is determined using the proportion mature at age, which can be applied to various dimensions of the population state.

Table 1: Partitions of the state object that are fixed inputs and the likely minimum and maximum input for each partition. The notation used for the partitions is also shown.

Partition (notation)	Dimension		Description
	Min	**Max**	
Age (a)	1	251	Age classes ranging from 0 to 250. Halibut will likely use 0 to 30 and age always starts at zero. A capital A indicates the maximum age
Sex (s)	1	3	Sex, which includes female, male, and unsexed, in that order, labeled 1, 2, and 3.
Time (t)	0	∞	A minimum and maximum time-step (e.g., year) is input by user. The difference +1 determines the number of time-steps. These are not projected time-steps, but time-steps modelled to condition the OM. A time-step will typically be a year, but specific points in time (e.g., beginning, middle, or end of the year) may be noted in a superscript (see below).
Region (r)	1	∞	Number of spatial regions with movement between
Area within Region (r_l)	1	∞	Number of areas within a region. Movement is not modelled between areas within a region.
Fishery (f)	1	∞	Number of fisheries and surveys. These are defined to operate at the region or area level.

The state object is the key component of the population dynamics and must contain sufficient information to determine the population dynamics as well as any intermediate calculations, such as fishery catches. In this implementation, there may be four partitions, but some operating models may have a state object partitioned with fewer elements, effectively eliminating that dimension. For example, a single-sex, single-area model would simply be a matrix of years and ages. Including maturity as a fifth potential state is a possible future improvement.

2.2 Notation

Notation of the variables in the operating model uses the concept of defining a quantity of the population (such as numbers or biomass), subscripted by various characteristics (intrinsic and extrinsic) and superscripted by specific concepts (such as spawning or exploitable). The subscripts reflect the intrinsic and extrinsic characteristics of the population by listing the intrinsic characteristics first (age and sex), followed by the extrinsic characteristics (time, region/area, and fishing sector). The possible subscripts are defined in Table 1 and are always subscripted in the order presented in those tables. For example, the numbers for age and sex in a year and region is $N_{a,s|t,r}$. When a subscript is not included, it is implied that the quantity is a summation over that index (or the index does not apply, as in the case of fishing sector) and ambiguity will be alleviated using the letter associated with the index when necessary (e.g., $N_{s=1|t=1}$ is the number of females in year 1 summed over all ages and regions).

Variables specific to a fishing sector (f) include a subscript for that sector at the end. For example, the catch-at-age for females from sector f in year 1 and region 2 would be notated as $C_{a,1|1,2,f}$. Fishery sectors operate at the region or area level.

Finally, superscripts are used to notate specific concepts such as spawning biomass, which would be notated as $B_{s=1|y=1}^{sp}$ to represent the spawning biomass for females in year 1 over all regions. Additionally, a superscript that is a number between 0 and 1 indicates the time in the year that the quantity is calculated. For example, $B^{sp,0}$, $B^{sp,0.5}$, $B^{sp,1}$ would be the spawning biomass calculated at the beginning of the year, middle of the year, and end of the year, respectively. Possible superscripts and their definition are shown in Table 2. Appendix I presents notation for many parameters.

Table 2: Superscripts for variables and their meaning.

Variable	Description
R	Related to recruitment at age zero
ma	Mature
sp	Spawning. Most often used with B^{sp} to represent spawning biomass.
sr	Selected and retained referring to the fish that are landed by a fishery sector.
n	Numbers. Indicates that a quantity, such as catch, is in numbers (C^n). Note that if a superscript is not used on catch, it is in weight.
'	Denotes update made to numbers-at-age after partial timestep is complete, which includes the effect of movement but not mortality.
"	Denotes update made to numbers-at-age at the end of the timestep after natural and fishing mortality.
Number *to 1*	*0* A number between zero and 1 (inclusive) indicates the time within the year. For example, 0 indicates beginning of the year, 0.5 indicates middle of the year, and 1 indicates end of the year.

2.3 Population dynamics

The population dynamics are modelled as an age-structured annual process accounting for changes in the numbers-at-age for each partition within the state (e.g. age and sex).

The sequence of processes from the start of the time-step (typically annual) is

1. age increment,

2. recruitment,

3. movement,

4. mortality,

    a. portion of natural mortality,

    b. fishing mortality for one or more sectors,

    c. portion of natural mortality,

    d. fishing mortality for one or more sectors,

    e. etc., until a full time-step of natural mortality has been applied,

5. spawning.

The state object ($N_{a,s|t,r}$) is updated at three different points in the annual process, and superscripts note the time point.

N	:	Beginning of the time-step after age increment and recruitment of age 0.
N'	:	After movement before mortality.
N''	:	End of the time-step, after all natural and fishing mortality.

At any point in time, the biomass can be calculated from numbers-at-age ($N_{a,s|t,r}$) and weight-at-age ($W_{a,s|t,r}$).

$$B_{a,s|t,r} \quad = \quad N_{a,s|t,r}W_{a,s|t,r} \tag{1}$$

Various partitions of biomass may be desired. For example, spawning biomass is the weight of spawning fish, and selected biomass is the weight of fish available to a specific fishery. These various types of biomass will be defined in the sections below and will be noted with a superscript. For example, spawning biomass is B_y^{sp}.

This section describes the technical specifications of the general population dynamics and how the historical population can be modelled given inputs such as catch and weight-at-age, as well as parameters that may be fixed or estimated. Conditioning the operating model is the process of determining the range of parameters and hypotheses that describe observations. Projecting the population involves defining random and fixed processes such as recruitment and changes in weight-at-age.

2.3.1   Age increment
The numbers-at-age at the beginning of the time-step with an annual time-step is obtained by incrementing the previous time-step's age class to one time-step older and calculating recruitment for age 0. A plus-group is defined at age A where all subsequent ages are accumulated.

$$N_{a,s|t,r} = \begin{cases} R_{s|t,r} & a = 0 \\ N_{a-1,s|t-1,r} & 1 \le a < A \\ N_{a-1,s|t-1,r} + N_{A,s|t-1,r} & a = A \end{cases} \tag{2}$$

2.3.2   Recruitment
Recruitment is a function of the spawning biomass calculated from either the end of the previous time-step or the beginning of the current time-step. See Section 2.3.6 for a description of spawning biomass.

$$R_{s|t,r} \quad = \quad p_{t,r}^R \times p_s^R \times f(B_{s=1}^{sp}) \times e^{(\varepsilon_t - b_t \frac{\sigma_R^2}{2})} \times e^{I_t \delta} \tag{3}$$

where $p_{t,r}$ is the proportion recruiting to region r in time-step t, p_s is the proportion of sex s (typically 0.50), $f(B_{s=1}^{sp})$ is the equilibrium stock-recruit relationship using either the end of the previous time-step or beginning of the current time-step spawning biomass (superscripts) for females, e^{ε_t} is the annual deviation in recruitment for time-step t, b_t is a bias-correction multiplier for time-step t (Methot & Taylor, 2011), and $e^{I_t \delta}$ is an overall adjustment for changes in recruitment due to regime shifts.

2.3.2.1   Density-dependent recruitment
Density-dependence in the spawner-recruit relationship is modelled using a Beverton-Holt formulation.

$$f(B_{s=1|t-1}^{sp}) = \frac{B_{s=1|t-1}^{sp}}{a + b B_{s=1|t-1}^{sp}} \tag{4}$$

where the parameters a and b are determined from steepness (h), unfished equilibrium recruitment (R_0), and unfished equilibrium female spawning biomass (B_0^{sp}).

$$a = \frac{(1-h)B_0^{sp}}{4hR_0} \tag{5}$$

$$b = \frac{5h-1}{4hR_0} \tag{6}$$

Steepness (h) is a parameter noting the percentage of unfished equilibrium recruitment (R_0) that occurs when the female spawning biomass is 20% of unfished equilibrium female spawning biomass (B_0^{sp}). This can be shown using Equations (4) to (6), and assuming that female spawning biomass is 1/5th of unfished equilibrium female spawning biomass.

$$= \frac{\frac{1}{5}B_0^{sp}}{\frac{(1-h)B_0^{sp}}{4hR_0}+\frac{5h-1}{4hR_0}\left(1/_5 B_0^{sp}\right)}$$

$$= \frac{\frac{1}{5}}{\frac{1-h+1/_5 5h-1/_5}{4hR_0}}$$

$$= \frac{\frac{4}{5}hR_0}{\frac{4}{5}}$$

$$= hR_0$$

The same method can be used to show that B_0 results in R_0. An example Beverton-Holt stock-recruit curve with a steepness of 0.70 is shown in Figure 3.
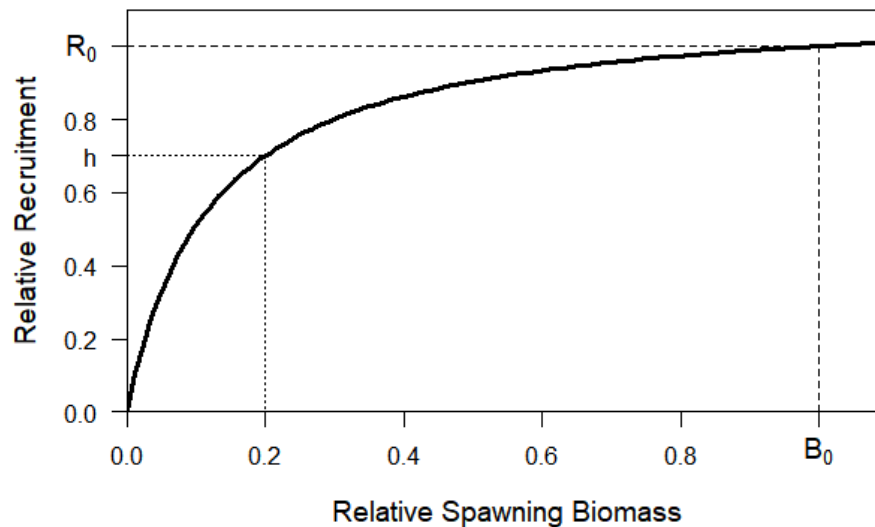
Figure 3: An example Beverton-Holt stock-recruit curve with a steepness (h) of 0.70.

The parameter for steepness is typically fixed because accurate estimation requires data informative of recruitment at low biomass levels and variability in recruitment often reduces the information content. The parameter R_0 is often estimated, and B_0^{sp} can be calculated from R_0 and other life history parameters. Given steepness, R_0, and B_0, the parameters a and b can be calculated.

2.3.2.2   Recruitment deviation

Recruitment varies around the stock-recruit curve, which is defined as mean recruitment. The distribution of recruitment is assumed to be lognormal and is parameterized using a Gaussian distributed deviate with mean or median equal to one and a variance notated as σ_R^2.

$$\varepsilon_{t,r} \sim N(\mu = 0, \sigma_R^2) \tag{7}$$

The arithmetic mean of the lognormal distribution is $e^{\mu + \sigma_R^2/2}$, and because R_0 is unfished equilibrium mean recruitment, a bias correction must be applied when simulating log deviates from a normal distribution with a mean/median equal to zero. As shown in Equation (3) $e^{\varepsilon_{t,r} - \sigma_R^2/2}$ is used where the bias correction is to subtract $\sigma_R^2/2$. This ensures that unfished equilibrium recruitment is, on average, R_0 (e.g., the mean of the biased corrected exponentiated deviate is equal to 1). Figure 4 shows an example simulation without fishing when bias correcting and not bias correcting, and Methot & Taylor (2011) present an analytical proof why bias correction is necessary.
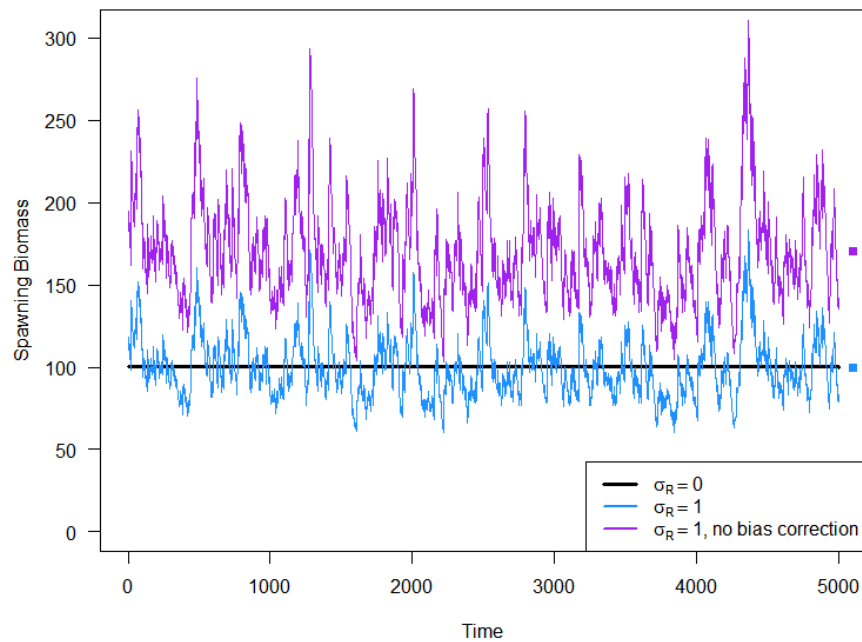

Figure 4: An example simulated projection of spawning biomass with no fishing mortality from an age-structured model with $\sigma_R = 1$ and bias-corrected recruitment deviates (blue line) and recruitment deviates not bias-corrected (purple line). A simulated trajectory with $\sigma_R = 0$ is shown by the flat black line, and the means of each simulated trajectory are shown by the appropriate colored square to the right.

Full bias-correction is necessary when simulating the fish population because the full lognormal distribution is used to simulate deviates, as shown in Figure 4. However, during estimation, information is reducing the uncertainty (i.e. distribution) around a deviation, and pulling it away from a value of zero. Therefore, a deviate without any information during estimation will be zero and not need bias correction, but a deviate that is fully informed (i.e., known exactly as in a simulation) will need full bias correction. In most estimation models, deviates are not often fully informed, and a partial bias-correction is necessary. Methot & Taylor (2011) provide a much more detailed discussion of this phenomenon. The parameter b_t is included in the equation for recruitment to allow for bias-correction if needed during estimation/conditioning.

The recruitment process is a coastwide process with age-0 recruits distributed to regions. Therefore, the deviates may be region-specific, but it may be more appropriate to use a single coastwide deviate for each year and simulate region-specific variability across time-steps with the parameters representing the proportion recruiting to each region ($p_{t,r}^R$). Using region-specific deviates and proportion of recruits may be confounding.

2.3.2.3 Recruitment distribution

Recruitment of age-0 fish to the population is determined from spawning biomass, and depending on the settlement process for a fish species and ocean dynamics, an age-0 fish may recruit a considerable distance from where spawning occurred. Furthermore, fish may migrate to spawning regions that are far from regions they occupied when not spawning. Therefore, the recruitment process is modelled assuming a coastwide spawning population (e.g., fish may spawn in regions where they are not present during the time of fishing) producing age-0 fish (recruits) throughout specified regions. The proportion of recruits in each region in each year is represented with the parameter $p_{t,r}^R$ as shown in equation (3) for recruitment, and $r - 1$ parameters need to be specified for each time-step because the rth parameter is one minus the sum of the specified parameters (i.e. $\sum_r p_{t,r}^R = 1$).

The parameters $p_{t,r}^R$ are modelled using a multinomial logit equation,

$$p_{t,r}^R = \frac{e^{\eta_{t,r}^R}}{\sum_r e^{\eta_{t,r}^R}} \tag{8}$$

$$\eta_{t,r}^R = \alpha_r^R + \beta_r^R x_t + \gamma_r^R x_t^2 \tag{9}$$

where α_r^R, $\beta_r^R x$, and γ_r^R are conditioned parameters, and x_t is a covariate that determines the time-vary aspects of recruitment distribution. The covariate x_t is currently linked to the environmental index I_t resulting in time-varying proportions recruited to each region r. The parameters $\beta_r^R x$, and γ_r^R determine the magnitude of the time-varying response.

The parameter η_r^R is fixed at zero for one region to make the proportion for all other regions relative to this fixed region. This can be accomplished by setting the α_r^R, $\beta_r^R x$, and γ_r^R parameters to zero for that region.

2.3.2.4 Recruitment link to an environmental variable

Recruitment is modelled (Equation (3)) using a stock-recruit relationship (i.e. Beverton-Holt, Equation (4)) that produces an average level of recruitment given current spawning biomass. Changes in the environment may change that average level of recruitment and is modelled using an environmental index (I_t) with the function $e^{I_t * \delta}$. The parameter δ is a covariate determining the effect of the environmental index on average recruitment.
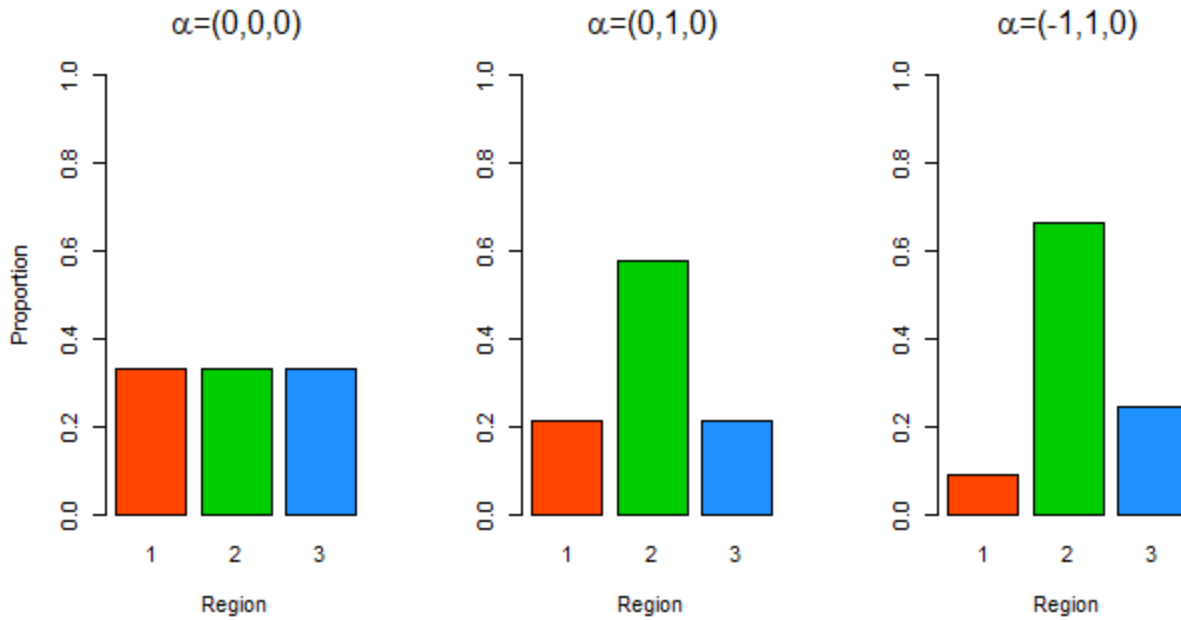
Figure 5. Example proportions for three regions determined from equations (8) and (9) with different α_r^R parameters. The third region is the reference regions with α_3^R set equal to zero. The parameters for $\beta_r^R x$ and γ_r^R are fixed at zero for all examples, therefore $\alpha = \eta$.

2.3.3 Movement

In its most simple form, movement (also called migration) is the proportion of individuals that move from region j to region k (individuals can only move among regions and movement among areas within regions is not explicitly modelled). The probability that the individual stays in its current region is equal to one minus the sum of the probabilities of moving out of the current region. Movement is specific to the partitions age, sex, time-step, and region.

One of the most common ways to model movement is using a transition matrix. Let $\Psi_{j \to k}$ be the instantaneous movement from region j to region k expressed as the proportion of the population (at age) in region j moving to region k. The diagonal of the transition matrix will be the proportion that stay in region j and the off-diagonals of $\Psi_{j \to k}$ will represent the proportions that move out of region j. The row of the matrix corresponds to j (from) and k corresponds to the column of the matrix (to). Each row of the transition matrix should sum to 1. Each dimension of the transition matrix will be equal to the number of regions. For example, let there be n regions ($R = 1 \dots n$), then the transition matrix for each age, sex, and time-step will look like:

$$\begin{bmatrix} \Psi_{R=1} & \Psi_{1 \to 2} & \cdots & \Psi_{1 \to n} \\ \Psi_{2 \to 1} & \Psi_{R=2} & \cdots & \Psi_{2 \to n} \\ \vdots & \vdots & \ddots & \vdots \\ \Psi_{n \to 1} & \Psi_{n \to 2} & \cdots & \Psi_{R=n} \end{bmatrix}$$

The numbers-at-age in region j after movement, for a given age, sex, and time-step, is determined from the following equation.

$$
\begin{aligned}
N'_{a,s,|t,r=j} &= N_{|r=j} - N_{|r=j}\sum_{k \neq j}\Psi_{a,s|t,j\to k} + \sum_{k \neq j}N_{|r=k}\Psi_{a,s|t,k\to j} \\
&= N_{|r=j}\left(1 - \sum_{k \neq j}\Psi_{a,s|t,j\to k}\right) + \sum_{k \neq j}N_{|r=k}\Psi_{a,s|t,k\to j} \\
&= N_{|r=j}\Psi_{a,s|t,j\to j} + \sum_{k \neq j}N_{|r=k}\Psi_{a,s|t,k\to j} \\
&= \sum_{k \in r}N_{|r=k}\Psi_{a,s|t,k\to j}
\end{aligned}
\tag{10}
$$

2.3.3.1 Movement parameters

There are two general options for the construction of the transition matrix:

1. entered as simple proportions in an array by time-step, age, sex, and region of origin, or

2. parameterize the proportions-at-age as a function of age and modify the parameters of the function for each time-step and sex.

Values can simply be entered for each movement probability-at-age (Equation (11)).

Values
$$
\Psi_{a,s|t,k\to j} = \begin{cases} 0 & a \leq \psi_0 \\ \psi_{v_a} & a < \psi_0 \end{cases}
\tag{11}
$$

where ψ_0 is the oldest age with a movement probability of zero before the first non-zero movement probability.

A parameterized approach is implemented using three options. These are functions called **constant** (Equation (12)), **exponential** (Equation (13)), or **two-sided exponential** (Equation (14)).

Constant
$$
\Psi_{a,s|t,k\to j} = \begin{cases} 0 & a \leq \psi_0 \\ \psi_c & a < \psi_0 \end{cases}
\tag{12}
$$

where ψ_c is a constant proportion for all ages greater than ψ_0.

Exponential
$$
\Psi_{a,s|t,k\to j} = \begin{cases} 0 & a \leq \psi_0 \\ \dfrac{e^{\psi_\lambda(a-\psi_0-1)} - 1}{\max\left(\psi_{a,s|t,k\to j}\right)} \times (\psi_{max} - \psi_{min}) & a > \psi_0 \end{cases}
\tag{13}
$$

where ψ_λ is the slope parameter of the exponential function, ψ_{min} is the minimum non-zero probability, and ψ_{max} is the maximum probability. The exponential equation is quite simple, but additional parts of Equation (13) have the purpose of standardizing the probabilities between ψ_{max} and ψ_{min}. A value of one is subtracted from the equation to shift the first non-zero age it to zero, as shown here.

$$
e^{\psi_\lambda(a-\psi_0-1)} - 1
$$

The maximum of the function over ages with non-zero probabilities is used to standardize the equation to not exceed one, as follows

$$\max(\psi_{a,s|t,k\to j}) = \max\left[e^{\psi_\lambda(A-\psi_0-1)} - 1\right]$$

and rescaled to be between ψ_{max} and ψ_{min} by multiplying by

$$(\psi_{max} - \psi_{min})$$

This provides a flexible parameterization that can mimic empirical observations and take on many different shapes as needed. Figure 6 shows an example outcome of the exponential for ages up to 30 with parameters ψ_0=2, ψ_λ=0.07, ψ_{max}=0.5 and ψ_{min}=0.05.
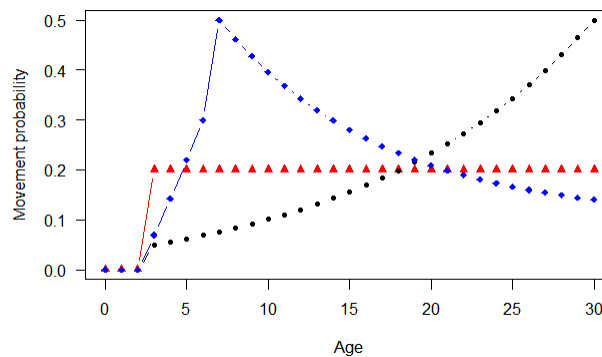

Figure 6. Example probabilities of movement at age using three parameterizations: constant (red triangles), exponential (black circles), and two-sided exponential (blue diamonds).

The two-sided exponential equation follows the parameterization of the exponential in Equation (13) with the addition of components to specify the two sides and ensure that they fall within a range specified by the parameters.

Two-sided

exponential

$$\Psi_{a,s|t,k\to j} = \begin{cases} 0 & a \le \psi_0 \\ \dfrac{e^{\psi_{\lambda L}(a-\psi_0)-1}}{\max(\psi_{a,s|t,k\to j})} \times \psi_{\mathrm{maxL}} & \psi_0 < a < \psi_{peak_L} \\ (\psi_{\mathrm{maxR}} - \psi_\alpha)e^{-\psi_{\lambda R}(a-(\psi_{peak_L}+1))} + \psi_\alpha & a > \psi_{peak_L} \end{cases} \quad (14)$$

where ψ_0 is the last age with a zero probability. The left side of the non-zero probabilities is commonly increasing and is defined by a slope parameter ($\psi_{\lambda L}$) and a parameter specifying the function value (ψ_{maxL}) at the oldest age defining the left side (ψ_{peak_L}). The left side is standardized to fall within the defined range as was described for the exponential equation above. The right side is commonly decreasing and is defined by a slope parameter ($\psi_{\lambda R}$), a parameter specifying the function value (ψ_{maxL}) at the first age defining the right side ($\psi_{peak_L} + 1$) and an asymptote of the function (ψ_α). Figure 6 shows an example outcome of the two-sided exponential for ages up to 30 with parameters ψ_0=2, ψ_{peak_L}=6, $\psi_{\lambda L}$=0.05, $\psi_{\lambda R}$=0.1, ψ_{maxL}=0.3, ψ_{maxR}=0.5, and ψ_α=0.1. Note that the left and right sides are discontinuous and there may be a considerable difference between the ages where they connect.

Overall, the following are the possible parameters in the four functions described by Equations (11) to (14) that may be specific to a sex, time, and region.

ψ_0: The oldest age with a movement probability of zero before the first non-zero movement probability. Therefore, all ages from age 0 to age ψ_0 do not move out the region they are in.

ψ_c: The constant non-zero probability of movement.

ψ_λ: The 'slope' of the exponential function in either the exponential function or associated with the left (λ_L) or right (λ_R) side of the double exponential.

ψ_{min}: The minimum non-zero probability of movement-at-age in the exponential function.

ψ_{max}: The maximum probability of the movement-at-age in the exponential function or for the left (max_L) or right (max_R) side of the double exponential function.

ψ_{peak_L}: The age at which the peak of the left ($peak_L$) side of the double exponential occurs. This is the transition between the left and right sides of the double exponential function. This parameter is an integer and the peak of the right side is one greater than ψ_{peak_L}.

ψ_α: The asymptote of the right side of the double exponential function.

ψ_{v_a}: Specific probability-at-age. Subsequent values after the last entered age are set to the last entered age.

2.3.4 Mortality

The operating model contains two types of mortality: natural mortality and fishing mortality. These are described below with definitions and mathematical equations. Total mortality, the summation of natural and fishing mortality, is noted as Z and is often modelled using a differential equation describing the instantaneous change with respect to a short period of time.

$$\frac{dN}{dt} = -Z \times N$$

Expanding to a single annual time step, the numbers in the next time-step, if mortality was the only process, are

$$N_{y+1} = N_y e^{-Z} \tag{15}$$

However, fishing mortality is often assumed to occur at a specific point in time.

$$N_{y+1} = N_y e^{-M}\left(1 - U_y\right) \tag{16}$$

where U_y is an annual exploitation rate. This formulation makes the calculations simpler, faster, and easier to interpret. The equations above are general mortality equations, and the specific equations related to natural and fishing mortality for the operating models are described below. We follow the FAO definition (http://www.fao.org/3/a0212e/a0212e12.htm) and call the fishing mortality process in Equation (15) instantaneous and that in Equation (16) finite.

2.3.4.1 Natural mortality

Natural mortality represents mortality from all sources other than fishing (e.g., natural causes, predation, and emigration out of the area being modelled) and may reflect some processes that are not specifically accounted for in the model. Many fisheries models assume that natural mortality is constant over time, which will likely capture the general trend in abundance, but natural mortality likely varies from time-step to time-step.

Therefore, the operating model allows for natural mortality that is age, sex, time-step, and region specific, but most applications will likely assume a single value for natural mortality for each sex.

2.3.4.2 Fishing mortality

Fishing mortality can be modelled using the Baranov catch equation (an instantaneous formulation as with natural mortality), but it is simpler, faster, and more interpretable to model fishing mortality as a finite exploitation rate (also called Pope's approximation). This assumes that fishing occurs at a specific point in time, which will be an important assumption to consider when the fishery operates year-round and at high mortality rates. For most applications, especially Pacific halibut with relatively low fishing mortality rates and a defined season, the exploitation rate is a useful approximation.

$$U_{|t,r,f} \quad = \quad \frac{C_{|t,r,f}}{B^{sr,p_f}_{|t,r,f}} \tag{17}$$

where $C_{|t,r,f}$ is the catch in time-step t and region r for sector f, and $B^{sr}_{|t,r,f}$ is the selected-and-retained biomass for that fishery. The time-point is the proportion of the time-step, p_f, at which the fishery occurs. The fishing sectors may operate at a scale finer than region, but region is used in the equations for fishing mortality. This assumes that a fish is available to any of the sectors in a region throughout an annual time step. Therefore, sectors are tracked at the region level, but may represent fishing in a particular area within a region (through selectivity and fishery timing, p_f). If a sector operates at a greater scale than region, that sector should be divided into region-specific sectors (a sector operates solely within a region). Therefore, the region and sector subscripts are redundant, but retained.

Selectivity represents the probability that a fish of a particular age will be caught by the sector. This is a combination of gear selection (e.g., the size of the hook or the width of mesh in a net) and availability (are fish of that age available in the area being fished). We do not separate these components and instead model them as a single probability. The selected proportions at age generally increase from young ages to older ages. However, they may also decline at the oldest ages, which is referred to as dome-shaped selectivity and may occur because older fish move out of the fishing area and become less available to the fishery, older fish may be able to avoid or escape the fishing gear, etc. Selectivity in this model is forced to have a maximum at one for at least one age. Therefore, the exploitation rate refers to the proportion of a fully selected age-class of fish removed from the population.

The proportion selected at age can be entered specifically for each age, modelled using a logistic formulation to asymptote at one (Equation (18)),

$$S_{a,s|t,r,f} \quad = \quad \frac{\zeta_{max,s|t,r,f}}{1 + 19^{(\zeta_{50,s|t,r,f}-a)/(\zeta_{a95,s|t,r,f}-\zeta_{a50,s|t,r,f})}} \tag{18}$$

or modelled using a double-normal function to allow for dome-shaped selectivity (Equation (19)).

$$S_{a,s|t,r,f} \quad = \quad \begin{cases} \zeta_{max,s|t,r,f}\dfrac{e^{-(a-\zeta_{peak,s|t,r,f})^2}}{2\zeta_{\sigma_L,s|t,r,f}} & a < \zeta_{peak,s|t,r,f} \\[2em] \mathrm{Max}\left[\zeta_{max,s|t,r,f}\dfrac{e^{-(a-\zeta_{peak,s|t,r,f})^2}}{2\zeta_{\sigma_R,s|t,r,f}},\zeta_{final,s|t,r,f}\right] & a \geq \zeta_{peak,s|t,r,f} \end{cases} \tag{19}$$

Parameters are described below. Examples of these two parameterizations are shown in Figure 7. Additional parameterizations may be introduced in the future. An option for all selectivity parameterizations is to define the age at which selectivity is zero for that age and all lower ages. This parameter is $\zeta_{zero,s|t,r,f}$.

There are three parameters in the logistic function for selectivity.

1. $\zeta_{a50,s|t,r}$: The age at which the probability of selection is 50% for sex s, at time t, and for sector f.

2. $\zeta_{a95,s|t,r}$: The age at which the probability of selection is 95% for sex s, at time t, and for sector f.

3. $\zeta_{max,s|t,r}$: The maximum probability of selection (asymptote) for sex s, at time t, and for sector f.
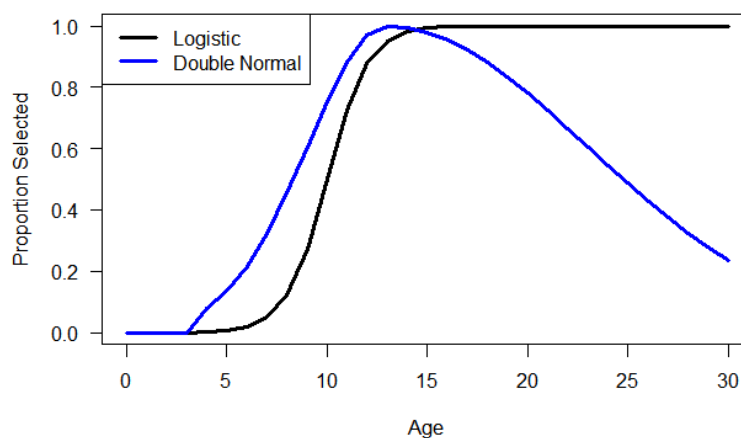

Figure 7: Examples of the logistic and double-normal parameterizations for selectivity

There are five parameters in the double normal function for selectivity.

1. $\zeta_{peak,s|t,r}$: The age at which the probability of selection is at its maximum for sex s, at time t, and for sector f. This is the division between the left and right sides of the function.

2. $\zeta_{\sigma_L,s|t,r}$: The standard deviation of the normal distribution for ages younger than the peak age ($\zeta_{peak,s|t,r}$). This side of the selection curve is referred to as the left side or ascending limb.

3. $\zeta_{\sigma_R,s|t,r}$: The standard deviation of the normal distribution for ages older than the peak age ($\zeta_{peak,s|t,r}$). This side of the selection curve is referred to as the right side or descending limb. To create an asymptotic selectivity ogive with the double normal this parameter would be fixed at a sufficiently large value.

4. $\zeta_{max,s|t,r}$: The probability at the age associated with the peak. This must be set at 1.0 for one of the sexes, but may be less than 1.0 for the other sex.

5. $\zeta_{final,s|t,r}$: The lowest value of the function on the right side of the function. The probability for ages that would be calculated less than this value are fixed at this value.

The availability of fish to a sector changes from year to year and changes may be made to gear for efficiency or to meet changes in regulation. Therefore, selectivity likely varies over time, hence the time subscript on the parameters and selectivity-at-age. Time-varying selectivity-at-age can be implemented by adjusting the parameters across time.

Specific terms are used to refer to fishery related quantities. Landings are the fish that are landed and quantified. These include, for example, commercial landings of a species greater than a size limit and fish retained in a recreational fishery. Captured fish refers to fish that are captured by fishing gear, of which some may subsequently survive if released. Some sources may refer to that as catch, but **the term catch in this document is synonymous with landings**. Of the captured fish that are subsequently released, some may die; this is called discard mortality. The sum of catch (i.e. landings) and discard mortality is the total fishing mortality. To model total fishing mortality an exploitation rate, selectivity curve, and retention curve are needed (or discards that die can be modelled as its own fishery).

Retention-at-age represents the probability that a captured fish is retained. This curve typically increases from lower probabilities at younger ages and nearing one at older ages, but often does not reach exactly one at its peak to represent the occasional discarding or loss of older/larger fish in that fishery. Low retention of young fish may represent a minimum size limit or high-grading for larger/older fish. Low retention of older fish may represent a maximum size limit or high-grading for smaller/younger fish. Retention is used to calculate the proportion of fish-at-age that are released (one minus retention) and may suffer discard mortality.

Retention is parameterized using the same options as selectivity (direct input by age, logistic, or double-normal). The retention parameters are

1. $\eta_{a50,s|t,r}$: The age at which the probability of retention is 50% for sex s, at time t, and for sector f.

2. $\eta_{a95,s|t,r}$: The age at which the probability of retention is 95% for sex s, at time t, and for sector f.

3. $\eta_{max,s|t,r}$: The asymptote (maximum probability) of retention (ranges from 0 to 1).

There are five parameters in the double normal function for retention and one optional parameter.

1. $\eta_{peak,s|t,r}$: (Required) The age at which the probability of retention is at its maximum for sex s, at time t, for sector f.

2. $\eta_{\sigma_L,s|t,r}$: (Required) The standard deviation of the normal distribution for ages younger than the peak age ($\eta_{peak,s|t,r}$). This side of the retention curve is referred to as the left side or ascending limb.

3. $\eta_{\sigma_R,s|t,r}$: (Required) The standard deviation of the normal distribution for ages older than the peak age ($\eta_{peak,s|t,r}$). This side of the retention curve is referred to as the right side or descending limb. To create an asymptotic retention ogive with the double normal this parameter would be fixed at a sufficiently large value.

4. $\eta_{max,s|t,r}$: The asymptote (maximum probability) of retention (ranges from 0 to 1).

5. $\eta_{final,s|t,r}$: The lowest value of the function on the right side of the function. The probability for ages that would be calculated less than this value are fixed at this value.

The logistic function for retention is

$$T_{a,s|t,r,f} \quad = \quad \frac{\eta_{max,s|t,r,f}}{1 + 19^{(\eta_{50,s|t,r,f}-a)/(\eta_{a95,s|t,r,f}-\eta_{a50,s|t,r,f})}} \tag{20}$$

and the double-normal function for retention is

$$T_{a,s|t,r,f} \quad = \quad \begin{cases} \eta_{max,s|t,r,f} \dfrac{e^{-(a-\eta_{peak,s|t,r,f})^2}}{2\eta_{\sigma_L,s|t,r,f}} & a < \eta_{peak,s|t,r,f} \\[2em] \text{Max}\left[\eta_{max,s|t,r,f} \dfrac{e^{-(a-\eta)^2}}{2\eta_{\sigma_R,s|t,r,f}}, \eta_{final,s|t,r,f}\right] & a \geq \eta_{peak,s|t,r,f} \end{cases} \tag{21}$$

It is important to not confuse retention with selectivity. For fisheries that retain all fish, the retention curve would be one across all ages because selectivity accounts for the sector not catching younger fish. The resulting product of retention and selectivity is called the keep curve and represents the probabilities-at-age of fish that are captured and retained, thus kept and landed. Figure 8 shows examples of selectivity and retention curves, and the resulting keep curve.
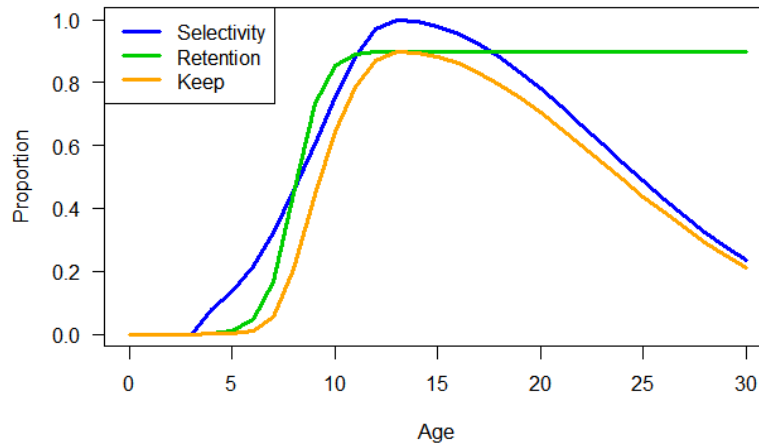

Figure 8: Examples of the double-normal parameterization for selectivity, a logistic parameterization for retention, and the resulting keep curve.

The sectors are assumed to operate at a very specific point of time defined as the proportion of the time-step (p_f). Some sectors will operate before others and will affect the abundance available later in the time-step. Therefore, the sequential operation of the sectors is accounted for by applying the probability that a fish survives sectors that occurred previously (catch and discard mortality). This necessitates determining only those sectors that occurred before the sector of interest.

Catch at age and sex in numbers (C^n) or weight (C) for a sector in an area can be determined from the numbers-at-age (N_a), natural mortality rate (M), exploitation rate (U_f), selectivity (S), proportion that are subsequently retained (T), mean weight-at-age (W), and the mortality from fisheries that occurred before the sector of interest. Appendix II presents details of this method as well as a method that does not take the sequence into account.

We notate the numbers-at-age and the biomass-at-age in a region and at a particular point in time in a time-step as $N_{a,s|t,r}^p$ and $B_{a,s|t,r}^p$, respectively, where the p superscript indicates the proportion of the time-step. Given this notation, the catch for a particular sector is

$$C_{a,s|t,r,f}^n = N_{a,s|t,r}^p U_{|t,r,f} S_{a,s|t,r,f} T_{a,s|t,r,f}$$
$$C_{a,s|t,r,f} = N_{a,s|t,r}^p W_{a,s,|t,r,f} U_{|t,r,f} S_{a,s|t,r,f} T_{a,s|t,r,f}$$

and the total catch for a sector is

$$C_{|t,r,f}^n = \sum_{a=0}^{A} \sum_{s} C_{a,s|t,r,f}^n \tag{22}$$

$$C_{|t,r,f} = \sum_{a=0}^{A} \sum_{s} C_{a,s|t,r,f} = U_{|t,r,f} B_{|t,r,f}^{sr,p} \tag{23}$$

where $B_{|t,r,f}^{sr,p}$ is the selected and retained biomass for sector f, and will be discussed later.

Discarded fish-at-age (fish caught but not retained) that suffer mortality after release (discard mortality) are an additional source of fishing mortality not accounted for in the retained catch. Discard mortality is calculated as

$$D_{a,s|t,r,f}^n = N_{a,s|t,r}^p U_{|t,r,f} S_{a,s|t,r,f} (1 - T_{a,s|t,r,f}) d_{a,s|t,r,f}$$
$$D_{a,s|t,r,f} = N_{a,s|t,r}^p W_{a,s|t,r,f}^d U_{|t,r,f} S_{a,s|t,r,f} (1 - T_{a,s|t,r,f}) d_{a,s|t,r,f}$$

where $d_{a,s|t,r,f}$ is the discard mortality rate (DMR) and $(1 - T_{t,a,s,f}) d_{t,a,s,r,f}$ is the proportion of selected fish that are released and do not survive. The weight-at-age ($W_{a,s|t,r,f}^d$) is notated with a d superscript indicating that the weight-at-age may differ for landings (catch) and discards. This is useful to mimic size-base discards in a model with age-based process. The summation of catch ($C_{|t,r,f}$) and discarded fish that die ($D_{|t,r,f}$) is the total mortality for sector f.

$$TM_{|t,r,f} = C_{|t,r,f} + D_{|t,r,f} \tag{24}$$

When modelling multiple fisheries occurring at different times, the calculation of N^p incorporates the mortality from fisheries that occurred previous to the sector of interest. The code may divide a time-step into sub-time-steps, but a more efficient method can be done using the probability that a fish survives an earlier sector in that time-step. The reader is referred to [Appendix II](#) for the details. The catch for a sector is

$$
\begin{aligned}
C_{a,s|t,r,f}^n = \; & N_{a,s|t,r} e^{-p_f M_{a,s|t,r}} \times \\
& \prod_{i \in p_j < p_f} \left[1 - U_{|t,r,i} S_{a,s|t,r,i} [T_{a,s|t,r,i} + (1 - T_{a,s|t,r,i}) d_{a,s|t,r,i}] \right] \times \\
& U_{|t,r,f} S_{a,s|t,r,f} T_{a,s|t,r,f}
\end{aligned}
\tag{25}
$$

$$C_{a,s|t,r,f} = C_{a,s|t,r,f}^n W_{a,s|t,r,f} \tag{26}$$

where

$$N_{a,s|t,r}^p = N_{a,s|t,r} e^{-p_f M_{a,s|t,r}} \prod_{i \in p_j < p_f} \left[1 - U_{|t,r,i} S_{a,s|t,r,i} [T_{a,s|t,r,i} + (1 - T_{a,s|t,r,i}) d_{a,s|t,r,i}] \right]$$

and incorporates the product of the probabilities-at-age of surviving fisheries that occurred prior to the sector of interest (f).

Discarded fish-at-age (fish caught but not retained) that suffer mortality after release (discard mortality) is calculated in a similar manner.

$$
\begin{aligned}
D^n_{a,s|t,r,f} \;=\; & N_{a,s|t,r}e^{-p_f M_{a,s|t,r}} \times \\
& \prod_{\substack{i \in p_j < p_f}} \left[1 - U_{|t,r,i}S_{a,s|t,r,i}\big[T_{a,s|t,r,i} + (1 - T_{a,s|t,r,i})d_{a,s|t,r,i}\big]\right] \times \\
& U_{|t,r,f}S_{a,s|t,r,f}(1 - T_{a,s|t,r,f})d_{a,s|t,r,f}
\end{aligned}
\tag{27}
$$

$$
D_{a,s|t,r,f} \;=\; D^n_{a,s|t,r,f}W^d_{a,s|t,r,f} \tag{28}
$$

where $d_{a,s|t,r,f}$ is the discard mortality rate (DMR) and $(1 - T_{t,a,s,f})d_{t,a,s,r,f}$ is the proportion of selected fish that are released and do not survive. The summation of catch ($C_{|t,r,f}$) and discarded fish that die ($D_{|t,r,f}$) is the total mortality for sector f (Equation (24)) and can be written as

$$
\begin{aligned}
TM^n_{|t,r,f} \;=\; & \sum_{a=0}^{A}\sum_{s} N_{a,s|t,r}e^{-p_f M_{a,s|t,r}} \times \\
& \prod_{\substack{i \in p_j < p_f}} \left[1 - U_{|t,r,i}S_{a,s|t,r,i}\big[T_{a,s|t,r,i} + (1 - T_{a,s|t,r,i})d_{a,s|t,r,i}\big]\right] \times \\
& U_{|t,r,f}S_{a,s|t,r,f}\big[T_{a,s|t,r,f} + (1 - T_{a,s|t,r,f})d_{a,s|t,r,f}\big]
\end{aligned}
\tag{29}
$$

$$
\begin{aligned}
TM_{|t,r,f} \;=\; & \sum_{a=0}^{A}\sum_{s} N_{a,s|t,r}e^{-p_f M_{a,s|t,r}} \times \\
& \prod_{\substack{i \in p_j < p_f}} \left[1 - U_{|t,r,i}S_{a,s|t,r,i}\big[T_{a,s|t,r,i} + (1 - T_{a,s|t,r,i})d_{a,s|t,r,i}\big]\right] \times \\
& U_{|t,r,f}S_{a,s|t,r,f}\big[W_{a,s|t,r,f}T_{a,s|t,r,f} + W^d_{a,s|t,r,f}(1 - T_{a,s|t,r,f})d_{a,s|t,r,f}\big]
\end{aligned}
\tag{30}
$$

The selected-and-retained biomass for sector f in the population is simply the mortality divided by the exploitation rate, but mortality is an input and selected-at-retained biomass must be calculated from selectivity (S), proportion retained (T), and mean weight-at-age (W) to determine the exploitation rate U_f (Equation (17)).

$$
B^{sr,p}_{|t,r,f} \;=\; \sum_{a=0}^{A}\sum_{s} N_{a,s|t,r}e^{-p_f M_{a,s|t,r}}S_{a,s|t,r,f}T_{a,s|t,r,f}W_{a,s|t,r,f} \tag{31}
$$

Following [Appendix II](#), natural and fishing mortality can be accounted for simultaneously, and the numbers-at-age in the next time-step, accounting for all mortality, are

$$
N''_{a,s|t,r} = N'_{a,s|t,r}e^{-M_{a,s|t,r}}\prod_{i=f}\left[1 - U_{|t,r,i}S_{a,s|t,r,i}\big[T_{a,s|t,r,i} + (1 - T_{a,s|t,r,i})d_{a,s|t,r,i}\big]\right] \tag{32}
$$

The exploitation rate is defined to be between zero and one, but it is possible that the exploitation rate may exceed one if the calculated exploitable biomass is less than the fixed input catch for a sector. If the exploitation rate for a specific sector exceeds 1, a negative population size may occur. Therefore, a maximum exploitation rate (U_{max}) must be specified, which is realistically less than one. If the exploitation rate for a sector exceeds the defined maximum, the exploitation rate for that sector should be set to the defined maximum. When this adjustment occurs, the predicted catch will be different than the input catch, and a penalty should be applied

since catches are considered observed inputs (not data with error). This penalty will be discussed in a later section on conditioning.

2.3.5 Maturity
Maturity and spawning may be separated into two separate states with maturity being a part of the state object, and the numbers of mature fish specifically tracked as part of the state. However, this operating model does not partition maturity in the state, but instead simply determines the numbers of mature fish from mature proportions-at-age (called the maturity curve).

$$N_{a,s|t,r}^{ma} = N_{a,s|t,r}\Omega_{a,s|t,r} \tag{33}$$

2.3.5.1 Maturity functional forms and parameters
The maturity curve (Ω) may be an empirical vector of proportions input by the user from externally estimated data. Alternatively, the vector or proportions may be determined from a functional form, such as a logistic equation, with appropriate parameters defined.

$$\Omega_{a,s|t,r} = \frac{\omega_{max,s|t,r}}{1 + 19^{(\omega_{50,s|t,r}-a)/(\omega_{a95,s|t,r}-\omega_{a50,s|t,r})}} \tag{34}$$

There are three parameters in this asymmetric logistic function.

1. $\omega_{max,s|t,r}$: The asymptote (maximum proportion) mature (ranges from 0 to 1).

2. $\omega_{a50,s|t,r}$: The age at which the proportion mature equals 50% of the asymptote for sex s, at time t, and in region r.

3. $\omega_{a95,s|t,r}$: The age at which the proportion mature is 95% of the asymptote for sex s, at time t, and in region r. Must be greater than $\omega_{a50,s|t,r}$.

2.3.6 Spawning biomass
The number of spawning individuals is the number that are mature at each age times the proportion spawning at each age. This allows for the accounting of individuals that are mature (able to produce gametes) but are not actively spawning in that time-step (e.g. skip spawning), and those that are mature and actively spawning in that time-step.

$$N_{a,s|t,r}^{sp} = N_{a,s|t,r}^{ma}\Phi_{a,s|t,r} \tag{35}$$

The spawning biomass (B^{sp}) is calculated as follows.

$$B_{|t,r}^{sp} = \sum_{a=0}^{A}\sum_{s} N_{a,s|t,r}^{sp}W_{a,s|t,r} \tag{36}$$

where $W_{a,s|t,r}$ is the population weight-at-age for that age, sex, time-step, and region at the beginning or end of the time-step as specified for the time of spawning.

Most sex-specific stock assessments account for only the female spawning biomass, which would simply be

$$B_{s=1|t,r}^{sp} = \sum_{a=0}^{A} N_{a,s=1|t,r}^{sp}W_{a,s=1|t,r} \tag{37}$$

2.3.6.1 Spawning proportion parameters

The proportion-at-age spawning (Φ) is a vector of proportions-at-age input by the user from externally estimated data. Typically, this vector contains a value of 1 for all ages because there is currently a paucity of information for many fish stocks.

2.3.7 Size-at-age

Growth is not modelled specifically (e.g. length-at-age), but weight-at-age is used to calculate biomass-at-age from numbers-at-age. Mean weight-at-age, sex, and region for a particular time-step and sector ($W_{a,s|t,r,f}$, which will simply be referred to as weight-at-age regardless of the various partitions), is input by the user. Fishery-specific weight-at-age are used because selectivity may operate on the larger fish of a certain age, resulting in a larger weight-at-age than in the population. Weight-at-age for discards is specified for fleets that model retention to allow for different size selection between discards and landings.

A random process is used for projecting variability in weight-at-age and is discussed below.

2.3.8 Initial population

The initial population is the partitioned population numbers at the start of the first modelled time-step, and is based on unfished equilibrium recruitment (R_0) with three potential adjustments.

1. An overall adjustment ($e^{\delta_{|I}}$) that changes R_0 (i.e., the overall scale of recruitment) and could mimic a different regime that influenced the initial population.

2. Cohort (a) specific adjustments to account for recruitment variability ($\varepsilon_{a|I}$).

3. Adjustments by age to account for an average level of fishing that occurred before the initial time-step: $\prod_f \left[1 - U_{|t,r,f} S_{a,s|t,r,f} \left[T_{a,s|t,r,f} + (1 - T_{a,s|t,r,f}) d_{a,s|t,r,f}\right]\right]$.

Calculating the initial equilibrium population size is not a simple calculation when region is in the partition and initial recruitment deviations are used. It is easiest to build up the population sequentially by each cohort that makes up the initial population using the sequence of processes described above: recruitment, movement, and mortality. This is time-consuming but is only done when starting a projection.

The number at age 0 for the cohort that is age a in the initial time-step (I) for each sex and region is

$$
N_{0,s|I-a,r} = \\
p_s \, p_{a|I,r} \, e^{\delta_{|I}} R_0 \, e^{\left(\varepsilon_{a|I} - \frac{\sigma_R^2}{2}\right)} \prod_f \left[1 - U_{|I,r,f} S_{0,s|I,r,f} \left[T_{0,s|I,r,f} + (1 - T_{0,s|I,r,f}) d_{0,s|I,r,f}\right]\right]
\tag{38}
$$

where p_s is the proportion of sex s at birth ($\sum_s p_s = 1$) and $p_{a|I,r}$ is the proportion of cohort a recruiting to region r in the initial time-step ($\sum_r p_{|I,a,r}$). It is assumed that there is a single selectivity curve for the initial time period that applies equally to all cohorts and a constant exploitation rate for all cohorts over their life-span before the initial time-step.

The equation above calculates the number for each cohort when they were age 0 prior to the initial time-step. To calculate the numbers-at-age in the initial time-step, the annual process for each cohort is iterated up to the age that each cohort would be in the initial time-step. For example, to calculate the cohort that is age 3 in the initial population, first determine the number of that cohort that were born into the population three time-steps prior. Then, the population dynamics would apply to that cohort for three iterations (0 to 1, 1 to 2, and 2 to 3) to determine the numbers in that cohort at age 3 in the initial time-step. Therefore, the annual process for the cohort that is age a in the initial time-step is iterated from $i = a \dots 1$ in the following equations. It begins by incrementing the annual process.

$$N_{a-i+1,s|I-i+1,r} \quad = \quad N_{a-i,s|I-i,r} \tag{39}$$

Then, movement from region j to k is applied. The subscripts for age, sex, and time-step are dropped for clarity in the derivation below but are noted in the final equation. Also note that the movement-at-age, Ψ, does not change in time-steps prior to the initial time-step.

$$
\begin{aligned}
N'_{a-i+1,s|I-i+1,j} \quad &= \quad N_{|j} - N_{|j} \sum_{k \neq j} \Psi_{|j \to k} + \sum_{k \neq j} N_{|k} \Psi_{|k \to j} \\
&= \quad N_{|j} \left(1 - \sum_{k \neq j} \Psi_{|j \to k} \right) + \sum_{k \neq j} N_{|k} \Psi_{|k \to j} \\
&= \quad N_{|j} \Psi_{|j \to j} + \sum_{k \neq j} N_{|k} \Psi_{|k \to j} \\
&= \quad \sum_{k \in r} N_{a-i+1,s|I-i+1,k} \Psi_{a-i+1,s|I,k \to j}
\end{aligned}
\tag{40}
$$

Finally, natural and fishing mortality is applied. Subscripts for age, sex, and time-step are dropped for clarity, but are the same as in the left side of the equation unless indicated (e.g. M, U, S, T, and d).

$$N''_{a-i+1,s|I-i+1,r} = N'_{|r} e^{(-M_{|I,r})} \prod_f \left[1 - U_{|I,r,f} S_{|I,r,f} \left[T_{|I,r,f} + (1 - T_{|I,r,f}) d_{|I,r,f} \right] \right] \tag{41}$$

The process is depicted in two different views in Table 3 and Table 4.

Table 3: A first illustration of how the initial population is calculated from previous cohort sizes. Cohorts at different ages are along diagonals.

		$U_{t=I-5}$	$U_{t=I-4}$	$U_{t=I-3}$	$U_{t=I-2}$	$U_{t=I-1}$	$U_{t=I}$
Selectivity		$I-5$	$I-4$	$I-3$	$I-2$	$I-1$	I
$S_{a=0}$		$coh5_{a=0}$	$coh4_{a=0}$	$coh3_{a=0}$	$coh2_{a=0}$	$coh1_{a=0}$	$coh0_{a=0}$
$S_{a=1}$			$coh5_{a=1}$	$coh4_{a=1}$	$coh3_{a=1}$	$coh2_{a=1}$	$coh1_{a=1}$
$S_{a=2}$				$coh5_{a=2}$	$coh4_{a=2}$	$coh3_{a=2}$	$coh2_{a=2}$
$S_{a=3}$					$coh5_{a=3}$	$coh4_{a=3}$	$coh3_{a=3}$
$S_{a=4}$						$coh5_{a=4}$	$coh4_{a=4}$
$S_{a=5}$							$coh5_{a=5}$

This method may not be at the exact equilibrium conditions due to approximations such as the plus group when movement occurs. Therefore, the user may enter a number of years for which the population is simulated without fishing to bring all age-classes in all regions to equilibrium.

Table 4: A second illustration of how the initial population is calculated from previous cohort sizes.

		Years before Initial						
		$\ldots$	$I-5$	$I-4$	$I-3$	$I-2$	$I-1$	I
Cohort								$coh0_{a=0}$
							$coh1_{a=0}$	$coh1_{a=1}$
						$coh2_{a=0}$	$coh2_{a=1}$	$coh2_{a=2}$
					$coh3_{a=0}$	$coh3_{a=1}$	$coh3_{a=2}$	$coh3_{a=3}$
				$coh4_{a=0}$	$coh4_{a=1}$	$coh4_{a=2}$	$coh4_{a=3}$	$coh4_{a=4}$
			$coh5_{a=0}$	$coh5_{a=1}$	$coh5_{a=2}$	$coh5_{a=3}$	$coh5_{a=4}$	$coh5_{a=5}$
		$\ldots$	$\ldots$	$\ldots$	$\ldots$	$\ldots$	$\ldots$	$\ldots$

2.3.8.1 *Summary of initial population numbers*
To summarize how the initial numbers in the partitions are completed, pseudocode is provided below.

1. Determine the initial number of age zero ($i = 0$) fish for the cohort ("*coh*" in the schematic representation of Table 3 and Table 4) of age a, where $a = 0,1,2,\ldots,nA$. The n is a multiplier on the plus group age A to simulate beyond the plus group to ensure the dynamics of the plus group are correct.

2. Loop over $a = 1,2,\ldots,nA$. For each a,

3. loop over $i = a, a-1, \ldots, 2,1$ applying ageing, movement, and mortality equations to build up the initial numbers for each cohort at age a.

4. sum numbers over $a = A, A+1, \ldots, nA$ to create the plus group (A).

5. iterate the population without fishing through a user specified number of time-steps.

A value of 3 is typically used for n, but it depends on the plus group age and the time willing to spend iterating over ages.

2.3.8.2 *Calculation of other initial population values*
Initial spawning biomass (beginning or end of year) is calculated after the initial numbers-at-age are completed.

$$B_{|I,r}^{sp} \quad = \quad \sum_{a=0}^{A} \sum_{s} N_{a,s|I,r} \Omega_{a,s|I,r} \Phi_{a,s|I,r} W_{y,a,s,r} \tag{42}$$

2.4   Projecting the operating models

The closed-loop feedback between the OM and the MP occurs in the projection period. Various population processes occur with variability and interact with the application of the management procedure. Details of the projections are provided in Section 2.1 of IPHC-2020-SRB017-09 and in Section 2.1 of IPHC-2020-MSAB016-08.

The OM interacts with the management procedure in a close-loop simulation via four possible methods (some still in development).

1. The OM calls R scripts for application of the MP. The OM is not stopped but is paused while the R script completes it processing for that annual time step.

2. The OM is called from R, completely stopped with the state saved, and then restarted at previous state with the inputs from the MP to complete an annual time-step. This is currently under development.

3. The OM is self-sufficient for simple MPs such as constant catch.

4. OM and MPs are one executable and specified though JSON input files (in development).

2.4.1   Recruitment

Recruitment is simulated in the projections from an average recruitment determined from the stock-recruit relationship that is dependent on environmental conditions (Equation (3)). Deviations from average recruitment (ε_t) are randomly drawn from a lognormal distribution, and the environmental regime shift (I_t) may be simulated externally and provided in an input file. Recruitment occurs on a coastwide scale, determined from the coastwide spawning biomass, and is apportioned to defined regions ($p_{t,r}^R$).

2.4.2   Fishing mortality

Mortality limits are determined from the management procedure and may include various forms of implementation variability. These include specific fisheries not matching the exact mortality limits or the actual mortality limits being different than the mortality limits determined from the MP.

Currently, simulated fishing mortality is added to a JSON file and read into the OM. The code of the OM does not apply any variation to the fishing mortality, but variation may be added when applying the management procedure and allocating fishing mortality. This is done by determining the mortality limits and determining realized mortality. Realized mortality is then entered in the JSON file for use in the OM.

In the future, there may be options to apply implementation variability to the fishing mortality within the OM and to simulate time-varying selectivity for the fishing fleets.

2.4.3   Movement

Movement probabilities are used in projections and may be tied to the same environmental regime used for recruitment. This allows for different parameters to be used for each regime

2.4.4   Weight-at-age

Projected values of weight-at-age are read in as an input to the OM thus may be externally modelled as desired. Future options may include modelling weight-at-age within the OM and including sampling variability.

2.5   Reference Points

Unfished equilibrium spawning biomass at the start of the year is found using weight-at-age, maturity-at-age, natural mortality, and unfished, equilibrium recruitment (R_0). As with the method for determining the initial population, the unfished equilibrium spawning biomass is determined after simulating forward in time to ensure the value is at equilibrium.

Static unfished equilibrium spawning biomass (i.e. static B_0) requires the definition of many parameters (e.g., weight-at-age) that are likely time-varying, thus the spawning biomass will fluctuate without fishing. Dynamic unfished quantities are calculated by simulating a 'shadow' state alongside the fished state. All parameters (including deviations) are the same, except that the 'shadow' state does not have any fishing mortality. The additional processing time is minimal because the 'shadow' state is entirely processed in memory with almost negligible additional reading or writing to disk and the fishing processes are not called, which are typically a large part of the processing time. This is a measure of the stock size if fishing had not occurred and is useful to calculate a stock status that is reflective of the effect of fishing and not the environment.

The calculation of Total Mortality based on SPR is done using the bisection method to solve for the Total Mortality that produces the desired SPR given a defined tolerance. This method uses the most recent biological parameters when calculating SPR and iterates the calculations of the fished population to ensure that all age-classes are at an equilibrium state. This can be time-consuming but is an accurate method.

3 SPECIFICATIONS FOR THE PACIFIC HALIBUT MSE FRAMEWORK

The Management Strategy Evaluation for Pacific halibut is currently being used to investigate elements of management procedures that set a coastwide mortality limit (coastwide scale) and determine catch limits for each IPHC Regulatory Area (distribution of mortality limits, Figure 9). This requires a multi-area operating model with fleets represented within IPHC Regulatory Areas (Figure 10). The specifications for the current Pacific halibut MSE framework are provided below.
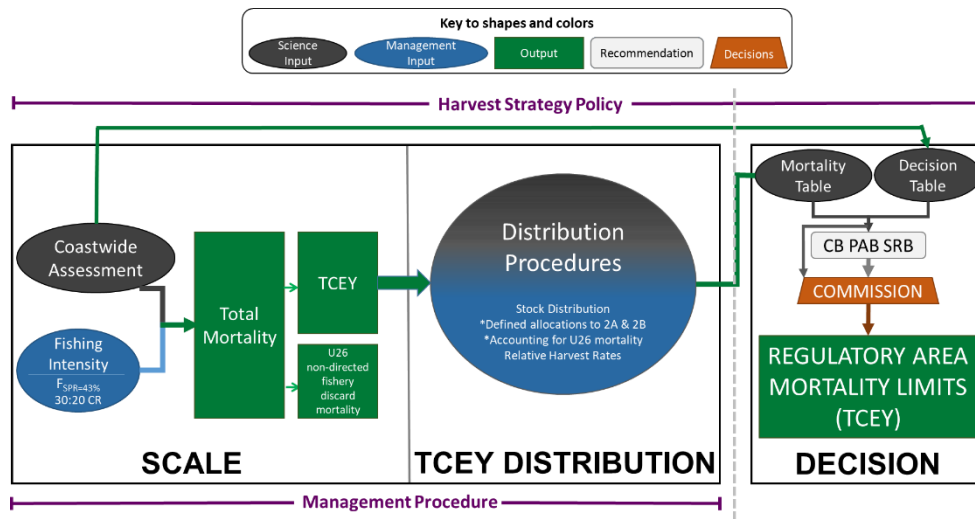

Figure 9. Illustration of the Commission interim IPHC harvest strategy policy (reflecting paragraph ID002 in IPHC-2020-CR-007) showing the coastwide scale and TCEY distribution components that comprise the management procedure. Items with an asterisk are interim agreements in place through 2022. The decision component is the Commission decision-making procedure, which considers inputs from many sources.
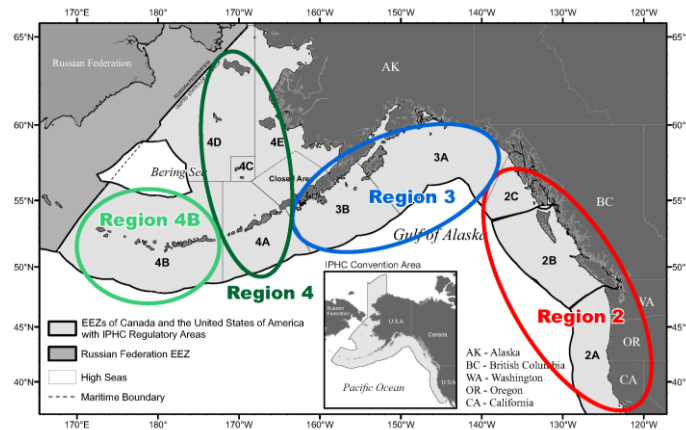
Figure 10: IPHC Regulatory Areas (grey shaded areas) and Biological Regions (colored circles).

3.1 Population and fishery spatial specification

The emerging understanding of Pacific halibut diversity across the geographic range of its stock indicates that IPHC Regulatory Areas should be only considered as management units and do not represent relevant sub-populations (Seitz, Farrugia, Norcross, Loher, & Nielsen, 2017). The structure of two of the four current Pacific halibut stock assessment models was developed around identifying portions of the data (fishery-independent and fishery-dependent data) that correspond to differing biological and population processes within the larger Pacific halibut stock. This approach, referred to as 'areas-as-fleets' is commonly used in stock assessments (Waterhouse, Sampson, Maunder, & Semmens, 2014), and was the approach recommended for inclusion in the ensemble developed in 2014 during the SRB review of models and used in all assessments since (Stewart & Martell, 2016).

Biological Regions (Figure 10) were therefore defined with boundaries that matched some of the IPHC Regulatory Area boundaries for the following reasons. First, data for stock assessment and other analyses are most often reported at the IPHC Regulatory Area scale and are largely unavailable for sub-Regulatory Area evaluation. Particularly for historical sources, there is little information to partition data to a portion of a Regulatory Area. Second, it is necessary to distribute TCEY to IPHC Regulatory Areas for quota management. If a Region is not defined by boundaries of IPHC Regulatory Areas (i.e. a single IPHC Regulatory Area is in multiple Regions) it will be difficult to create a distribution procedure that accounts for biological stock distribution and distribution of the TCEY to Regulatory Areas for management purposes. Further, the structure of the current directed fisheries does not delineate fishing zones inside individual IPHC Regulatory Areas, so there would be no way to introduce management at that spatial resolution. It is unlikely that there is a set of regions that accurately delineates the stock biologically since different aspects of the stock differ over varying scales, biological boundaries may shift over time, and movement occurs among Biological Regions.

To a certain degree, Pacific halibut within the same Biological Region share common biological traits different from adjacent Biological Regions. These traits include sex ratios, age composition, and size-at-age, and historical trends in these data may be indicative of biological diversity within the greater Pacific halibut population. Furthermore, tagging studies have indicated that within a year, larger Pacific halibut tend to undertake feeding and spawning migrations within a Biological Region, and movement between Biological Regions typically occurs between years (Webster, Clark, Leaman, & Forsberg, 2013; Loher & Seitz, 2006; Seitz, Loher, & Nielsen, 2007).

Given the goals to divide the Pacific halibut stock into somewhat biologically distinct regions and preserve biocomplexity across the entire range of the Pacific halibut stock, Biological Regions are considered by the IPHC Secretariat, and supported by the SRB (paragraph 31 IPHC-2018-SRB012-R), to be the best option for

biologically-based areas to meet management needs. They also offer an appropriate and parsimonious spatial separation for modeling inter-annual population dynamics.

However, as mentioned earlier, mortality limits are set for IPHC Regulatory Areas and thus directed fisheries operate at a smaller spatial scale than Biological Regions. Furthermore, since some fishery objectives have been defined at the IPHC Regulatory Area level, the TCEY will need to be distributed to that scale. Even though the population is modelled at the Biological Region scale, fisheries can be modelled at the IPHC Regulatory Area scale by using an areas-as-fleets approach within Biological Regions. This requires modelling each fleet with separate selectivities and harvest rates that operate on the biomass occurring in the entire Biological Region in each year. The following is a discussion of the pros and cons of this method.

First, modelling the population dynamics at the IPHC Regulatory Area scale would require intra-annual dynamics to be modelled, dividing the year into seasons to model movement between IPHC Regulatory Areas. There is evidence that such intra-annual movements occur (Loher & Seitz, 2006) and fisheries in adjacent IPHC Regulatory Areas may intercept the same pool of fish (Loher & Blood, 2009; Loher T. , 2011). Using Biological Regions assumes that all fisheries within a Region have access to the pool of Pacific halibut in that Region in that year. This greatly simplifies the calculations and eliminates the need to parameterize intra-annual movement. However, if a fishery does not interact with the pool of fish in a Biological Region, harvest rates determined for each fishery may be inaccurate because the biomass to which selectivity is applied would be incorrect, and some fisheries in the model may select ages/sizes of Pacific halibut that they commonly do not interact with. This is unlikely to occur and will have very little effect on the results of this MSE because harvest rates are not explicitly used in the management procedures (mortality limits are used for management) and similarity of age/size compositions were used to define Biological Regions.

Additionally, calculating statistics specific to IPHC Regulatory Areas requires assumptions about distribution of biomass within a Biological Region. For example, simulating the observed proportion of biomass in each IPHC Regulatory Area (e.g., to mimic the current interim management procedure) requires simulating a survey biomass for each IPHC Regulatory Area. Likewise, determining some objectives related to IPHC Regulatory Area may be difficult to calculate (such as the proportion of O26 fish in each IPHC Regulatory Area). The distribution of the population within a Biological Region is currently approximated assuming specified proportions of the population in each IPHC Regulatory Area within a Biological Region. These proportions are constant over ages and allows for the calculation of statistics specific to IPHC Regulatory Areas. Future improvements to the framework will allow for different options such as determining proportions from historically observed distributions and accounting for year to year variability.

Fisheries were defined by IPHC Regulatory Areas (or combinations of areas if fishing mortality in that area is historically small) and for five general sectors consistent with the definitions in the recent IPHC stock assessment (IPHC-2021-SA-01):

1. **directed commercial** representing the O32 mortality from the directed commercial fisheries including O32 discard mortality (from lost gear or regulatory compliance);

2. **directed commercial discard** representing the U32 discard mortality from the directed commercial fisheries, comprised of Pacific halibut discarded due to the minimum size limit;

3. **non-directed commercial discard** representing the mortality from incidentally caught Pacific halibut in non-directed commercial fisheries;

4. **recreational** representing recreational landings (including landings from commercial leasing) and recreational discard mortality; and

5. **subsistence** representing non-commercial, customary, and traditional use of Pacific halibut for direct personal, family, or community consumption or sharing as food, or customary trade.

Table 5 shows the summed mortality realized from 1992 through 2019 for each of these sectors by IPHC Regulatory Area or Biological Region. Thirty-three (33) fisheries were defined as a sector/area combination based on the amount of mortality in the combination, data availability, and MSAB recommendations (Table 6).

Table 5: Summed mortality (millions of net pounds) from 1992 through 2019 by sectors and IPHC Regulatory Area.

Year	2A	2B	2C	3A	3B	4A	4CDE	4B
Directed commercial	17.5	259.8	205.5	551.2	252.4	78.2	72.5	62.8
Directed commercial discard mortality	0.5	7.1	5.2	16.7	10.7	2.1	1.3	0.8
Non-directed discard mortality	11.8	12	4.5	73.6	36.2	39.2	128.6	16.2
Recreational	13.7	31.8	71.1	152.2	0.5	1.4	<0.1	<0.1
Subsistence	0.7	9.6	10.3	7.6	1	0.6	<0.1	2.4

3.2 Goals and objectives

The primary objectives used to evaluate MPs are presented in Appendix III.

3.3 Management procedures

3.3.1 Data and fishing mortality generation

Data generation is the code that simulates the data collection and analysis process from the operating model that are then used by the estimation model and MPs. Example data are survey indices, age-compositions, and stock distribution. It simulates the sampling process and can introduce variability, bias, and any other properties that are desired. For each year, the OM provides numbers-at-age in the stock by sex and region, numbers-at-age in the catch by sex, region and fishery sector, numbers-at-age available to each fishery sector at a specific point in time, selectivity-at-age by fishery sector, and weight-at-age by sex, region and fishery sector. From these outputs the data generation procedure generates catch-at-age data and survey indices for use in the EM, as well as stock distribution across Biological Regions and IPHC Regulatory Areas. In the attempt to mimic the data collection process carried out by the Commission as close as possible, data are first generated at the IPHC Regulatory Area level and then aggregated to Biological Regions or to the entire convention area (coastwide).

3.3.1.1 Proportion at age in the catch and in the survey.

Proportion-at-age in the catch (i.e. landings) by fishery sector are derived from the numbers-at-age available to each fishery sector at a specific point in time multiplied by the selectivity-at-age for each specific fishery sector. From this exploitable abundance-at-age the proportions-at-age are calculated.

$$p_{a,s|t,r}^{NAA} = \frac{N_{a,s|t,r}S_{a,s|t,f}}{\sum_{a=0}^{A} N_{a,s|t,r}S_{a,s|t,f}} \tag{43}$$

where $N_{a,s|t,r}$ are the numbers-at-age in the population available to a specific fishery f operating in region r, $S_{a,s|t,f}$ is the selectivity by age and sex for each year and fishery f. Observation error is implemented using a Dirichlet distribution with the scale parameter determined from the sample size as described below. This distribution has the same range and mean as a multinomial distribution, but its variance is controlled by the scale parameter. The generated proportion-at-age by fishery are then multiplied by the fishery total mortality in number, to calculate catch-at-age in numbers for each fishery. These catch-at-age are aggregated by the 5 main

sectors (i.e. directed commercial, recreational and subsistence, directed discard, non-directed discard, survey) to a coastwide level and used to calculate the coastwide proportions-at-age by sector to be used in the coastwide EM. In 2023, the MSE framework does not use an estimation model that requires proportions-at-age (see Section 3.3.3), thus these values are not currently calculated.

Table 6: The thirty-three fisheries in the OM, the IPHC Regulatory Areas they are composed of, and the 2019 mortality (millions of net pounds) for each.

Fishery	IPHC Regulatory Areas	2019 Mortality Mlbs	2019 Mortality tonnes
Directed Commercial2A	2A	0.89	404
Directed Commercial 2B	2B	5.22	2,368
Directed Commercial 2C	2C	3.67	1,665
Directed Commercial 3A	3A	8.16	3,701
Directed Commercial 3B	3B	2.31	1,048
Directed Commercial 4A	4A	1.45	658
Directed Commercial 4B*	4B	1.00	454
Directed Commercial 4CDE	4CDE	1.65	748
Directed Commercial Discards 2A	2A	0.03	14
Directed Commercial Discards 2B	2B	0.13	59
Directed Commercial Discards 2C	2C	0.06	27
Directed Commercial Discards 3A	3A	0.32	145
Directed Commercial Discards 3B	3B	0.15	68
Directed Commercial Discards 4A	4A	0.09	41
Directed Commercial Discards 4B	4B	0.03	14
Directed Commercial Discards 4CDE	4CDE	0.07	32
Non-directed Commercial Discards 2A	2A	0.13	59
Non-directed Commercial Discards 2B	2B	0.24	109
Non-directed Commercial Discards 2C	2C	0.09	41
Non-directed Commercial Discards 3A	3A	1.65	748
Non-directed Commercial Discards 3B	3B	0.48	218
Non-directed Commercial Discards 4A	4A	0.35	159
Non-directed Commercial Discards 4CDE	4CDE	3.50	1,588
Non-directed Commercial Discards 4B	4B	0.15	68
Recreational 2B	2B	0.86	390
Recreational 2C	2C	1.89	857
Recreational 3A	3A	3.69	1,674
Subsistence 2B	2B	0.41	186
Subsistence 2C	2C	0.37	168
Subsistence 3A	3A	0.19	86
Recreational/Subsistence 2A	2A	0.48	218
Recreational/Subsistence 3B	3B	0.02	9
Recreational/Subsistence 4	4A, 4CDE	0.06	27

*The small amount of recreational and subsistence mortality from IPHC Regulatory Area 4B is included in Directed Commercial 4B

3.3.1.2 Sample size

The number of fish aged for each fishery (sample size) in a specific year is used as the scale parameter for the Dirchlet distribution as a measure of variance, i.e., a higher sample size implies lower variance, and it is an input of the estimation model.

The sample size by Biological Region is generated directly using a fixed proportion of the total mortality by sector or total abundance within Biological Region (which assumes each fishery within a Biological Region samples at the same proportion):

- *sample size for the directed commercial, non-directed commercial discard mortality, recreational and subsistence sectors*: for each sector, the sample size is calculated using a fixed proportion of the total mortality (in numbers) by Biological Region and sector.

- *sample size for survey and directed commercial discard mortality sectors*: for each sector, the sample size is calculated using a fixed proportion of the available numbers-at-age by region.

The proportion chosen is based on an average of the sampling effort over the last 20 years. Resulting sample sizes are bounded within the maximum and minimum values observed historically for each fishery. The 2023 MSE framework does not currently require a sample size.

Survey NPUE and commercial WPUE.

The modelled Fishery Independent Setline Survey (FISS) NPUE ($I_{t,r}^{sur}$) and the commercial WPUE ($I_{t,r}^{comm}$) are needed for the distribution procedure at Biological Region and IPHC Regulatory Area levels. An MSE framework incorporating an estimation model with generated data would require the FISS NPUE and commercial WPUE at the coastwide level and possibly for each Biological Region, but these are not required for the 2023 MSE framework. The OM produces the numbers-at-age available to the survey and the numbers-at-age available to each directed commercial fishery. From these values, the abundance and biomass are determined for the survey and each fishery, noting that these are determined from abundance in the entire Biological Region.

Two types of indices are calculated: absolute and relative indices of abundance. The absolute indices of abundance are generated from the survey or fishery numbers-at-age in each Biological Region. The relative indices of abundance are calculated by multiplying the absolute index in each Biological Region by the regional catchability ($q_{t,r}$).

$$I_{t,r}^{surAll} = q_{t,r}^{sur} \sum_{a=0}^{A} N_{a,s|t,r,f} S_{a,s|t,f} \tag{44}$$

$$I_{t,r}^{comm} = q_{t,r}^{comm} \sum_{a=0}^{A} N_{a,s|t,r,f} S_{a,s|t,f} W_{a,s|t,f} \tag{45}$$

where $q_{t,r}^{sur}$ and $q_{t,r}^{comm}$ are the catchabilities coefficient for the survey and directed commercial fleet respectively for a specific region and year, $N_{a,s|t,r,f}$ is the sex-specific numbers-at-age available in each region and year to each fishery, $S_{a,s|t,f}$ is the sex-specific selectivity-at-age for a fleet in a specific year, and $W_{a,s|t,f}$ is the sex-specific weight-at-age for a each fishery in each year. Observation error is introduced through randomly generated lognormal deviates ($\varepsilon_{t,r}$).

$$\hat{I}_{t,r}^{sur} = I_{t,r}^{sur} e^{\varepsilon_{t,r}^{sur}} \tag{46}$$

$$\hat{I}_{t,r}^{comm} = I_{t,r}^{comm} e^{\varepsilon_{t,r}^{comm}} \tag{47}$$

Some of the harvest control rules use the over 32 inches (O32) stock distribution (in weight) at the Biological Region and IPHC Regulatory Area levels. Therefore, the numbers-at-age are multiplied by the probability of each age (by sex) being 32 inches or longer ($P_{O32,a,s|t}$) before determining the survey O32 WPUE. The probability of each age for each sex being 32 inches or longer was determined from weight-at-age and length-weight parameters in each Biological Region (see Section 3.3.2).

$$I_{t,r}^{surO32} = q_{t,r}^{sur} \sum_{a=0}^{A} N_{a,s|t,r,f} P_{O32,a,s|t} S_{a,s|t,f} W_{a,s|t,f} \tag{48}$$

Regional q is specified as relative to Biological Region 3. The weighted mean (where the weight is the survey bottom area and the commercial catch for the NPUE and WPUE, respectively) will equal the coastwide q. The proportion of each regional q relative to q in Biological Region 3 was arbitrarly fixed to the average of the last 20 years (Figure 11). However, the 2023 MSE framework only calculates absolute indices of abundance for use in determining stock distribution, which assumes that catchability is constant across Biological Regions.
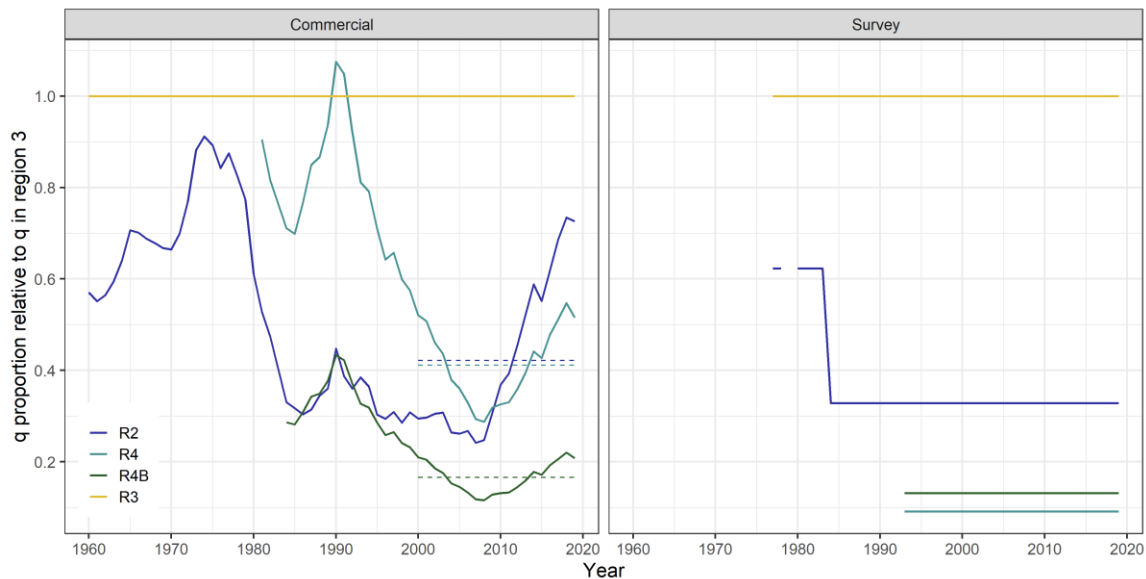

Figure 11: Proportion of each regional q relative to Biological Region 3 for the commercial WPUE (left) and the survey NPUE (right). The average of the years 2000 to 2019 is shown as a dotted line.

To derive the indices at the IPHC Regulatory Area level the regional abundance and biomass are partitioned using a recent 5-year average of the historical stock distribution (all-sizes or O32) within that region from the modelled FISS survey (Figure 12). The catchability is assumed to be equal for each IPHC Regulatory Area within a Biological Region.

Relative survey indices, proportions-at-age, and commercial indices are not currently used in the 2023 MSE framework because the estimation error is modelled in a simplistic way. Investigations continue to develop an EM with good performance when using these data within a fitted model.
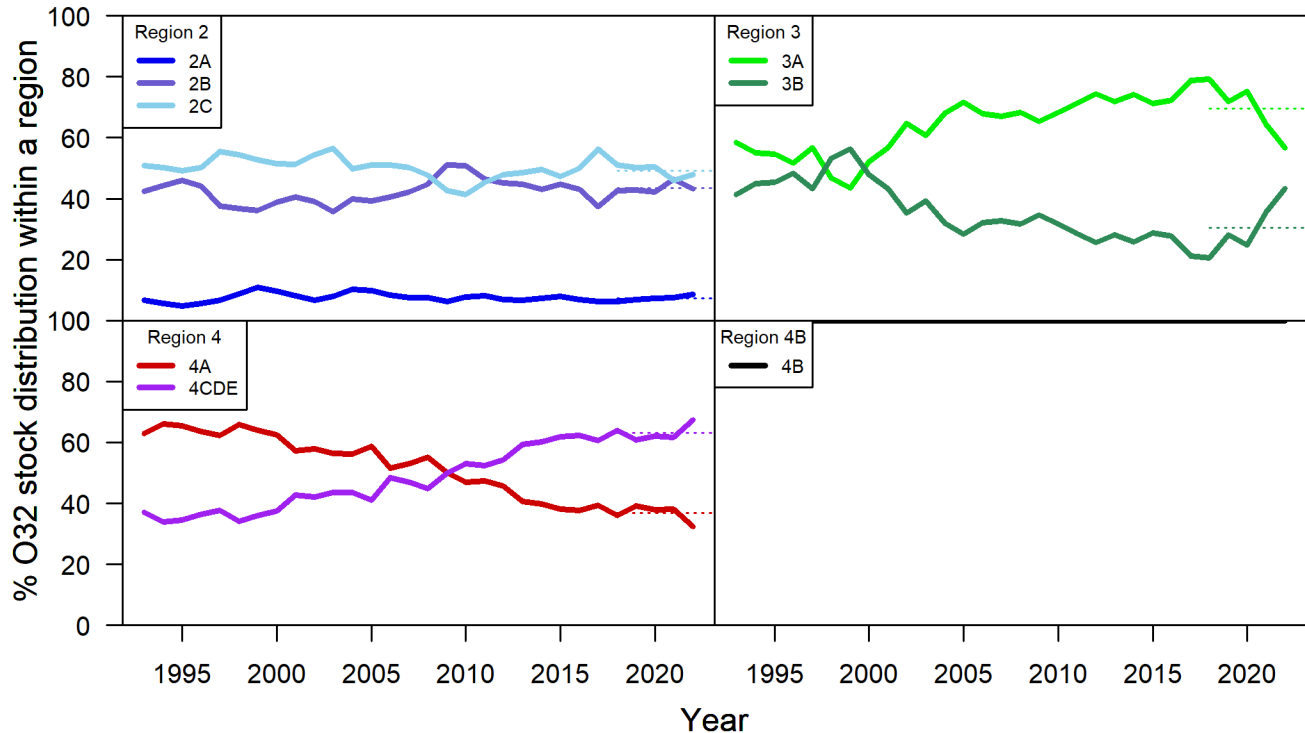

Figure 12: Proportion of O32 stock distribution in each IPHC Regulatory Area by Biological Region from the modelled FISS survey up to 2022. The recent 5-year average is shown as a dotted line.

Realized fishing mortality

The outputs of the management procedure are TCEY limits for each IPHC Regulatory Area, which then need to be allocated to the different sectors specific to the IPHC Regulatory Area. Mortality from each sector is determined from these limits with random variability introduced.

There are two parts to the allocation procedure: the calculation of the upcoming mortality limits by sector, and the calculation of the realized mortality by sector. The calculation of mortality limits is necessary because some sector's mortality limits are determined from the limits for other sectors. In the current framework, the calculation of the realized mortality differs from the calculation of the mortality limits for the non-directed discard, directed discard, subsistence, and unguided recreational mortalities. Mortality limits and realized mortality for the recreational and directed commercial sectors are assumed to be equal (i.e., no implementation error for these sectors).

The allocation procedure begins by subtracting the non-directed commercial O26 discard mortality by IPHC Regulatory Area from the corresponding IPHC Regulatory Area TCEY. The remainder is referred to as the directed TCEY for convenience (it is not used as a management quantity). The directed TCEY is then allocated to directed fishery sectors. Each IPHC Regulatory Area has a unique catch-sharing plan (CSP) or allocation

procedure, and these CSPs were matched as closely as possible. When the TCEY for an IPHC Regulatory Area is low, the CSP may deteriorate and alternative decisions may be necessary. At low TCEY, it is assumed that the sum of the directed non-FCEY components does not exceed the directed TCEY: this is evaluated sequentially removing the non-directed discard mortality, the subsistence mortality, and unguided recreational mortality (where available) from the TCEY. If any of these mortalities exceed the remaining TCEY, the remaining components are set to zero.

Non-directed commercial discard mortality: the U26 and O26 components of the non-directed discard mortality limit in the MP is calculated from previous years non-directed discard mortality for each IPHC Regulatory Area. However, the realized non-directed discard mortality is determined from a linear relationship between the non-directed discard mortality by region and the total biomass in that region. Given changes in non-directed commercial discard mortality in recent years the fit was forced through the year 2019. The realized non-directed discard mortality was then randomly drawn from the value determined from total biomass by region using a log normal distribution with a 20% CV (Figure 13). The non-directed commercial discard mortality by region is then distributed to IPHC Regulatory Area using the proportion of non-directed commercial discard mortality recently observed in each IPHC Regulatory Area.
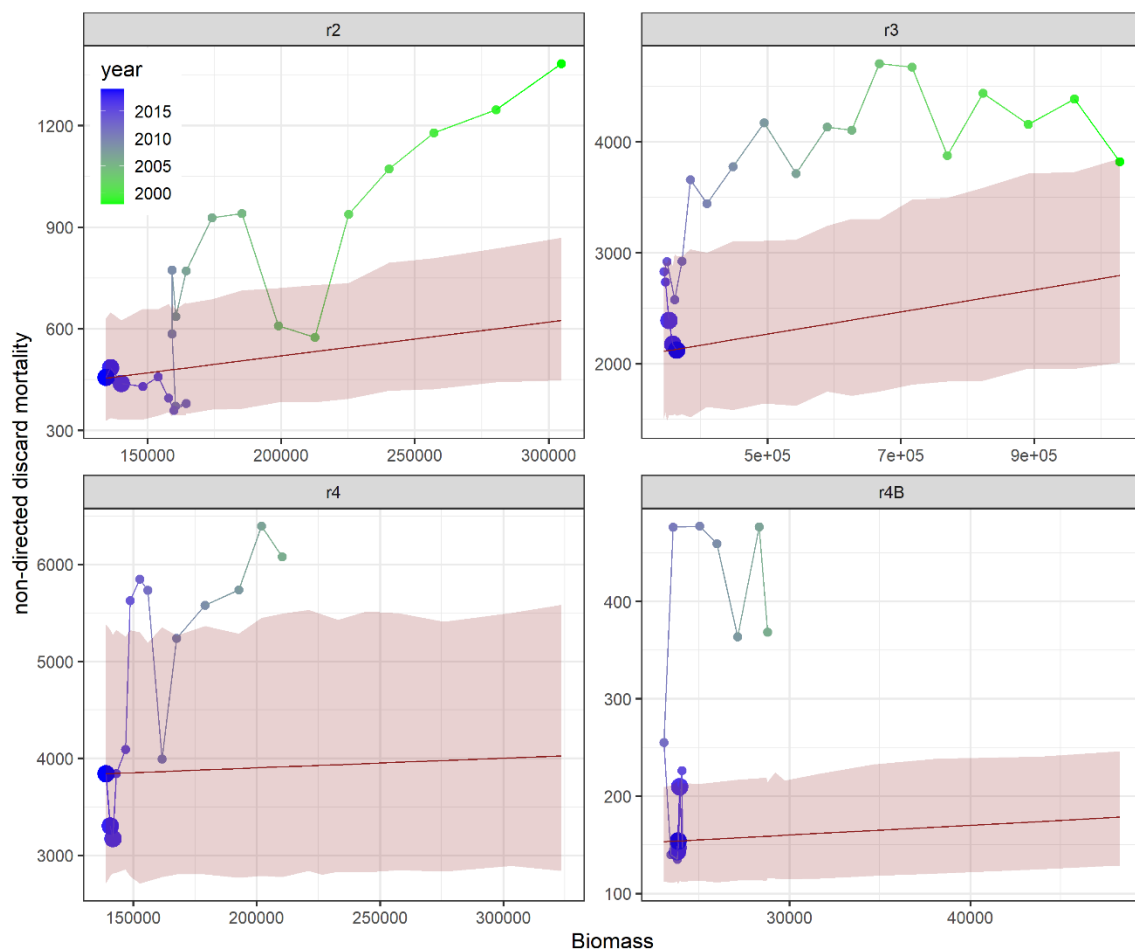

Figure 13. Non-directed commercial discard mortality plotted against total biomass from the conditioned multi-region OM. The colors in the points represent the sequence of time from 1998 to 2019. The years 2017–2019 are represented by larger dots. The red line represents the linear relationship used for predicting the non-directed discard mortality from the biomass. The shaded red area around it represents the 0.05 and 0.95 quantiles of the non-directed discard mortality simulated from a log-normal distribution with a 20% CV.

Directed commercial discard mortality: directed commercial discard mortality limits are calculated using the ratio of directed discard mortality to directed commercial mortality from the previous year. The realized directed discard mortality is modelled as a function of the directed commercial plus directed discard mortality and the weight at age 8 for a male Pacific halibut. The resulting proportion of directed discard mortality relative to different values of the commercial plus directed discard mortality is shown in Figure 14. A minimum of 0.05% of directed discard mortality over commercial plus directed discard mortality is applied.
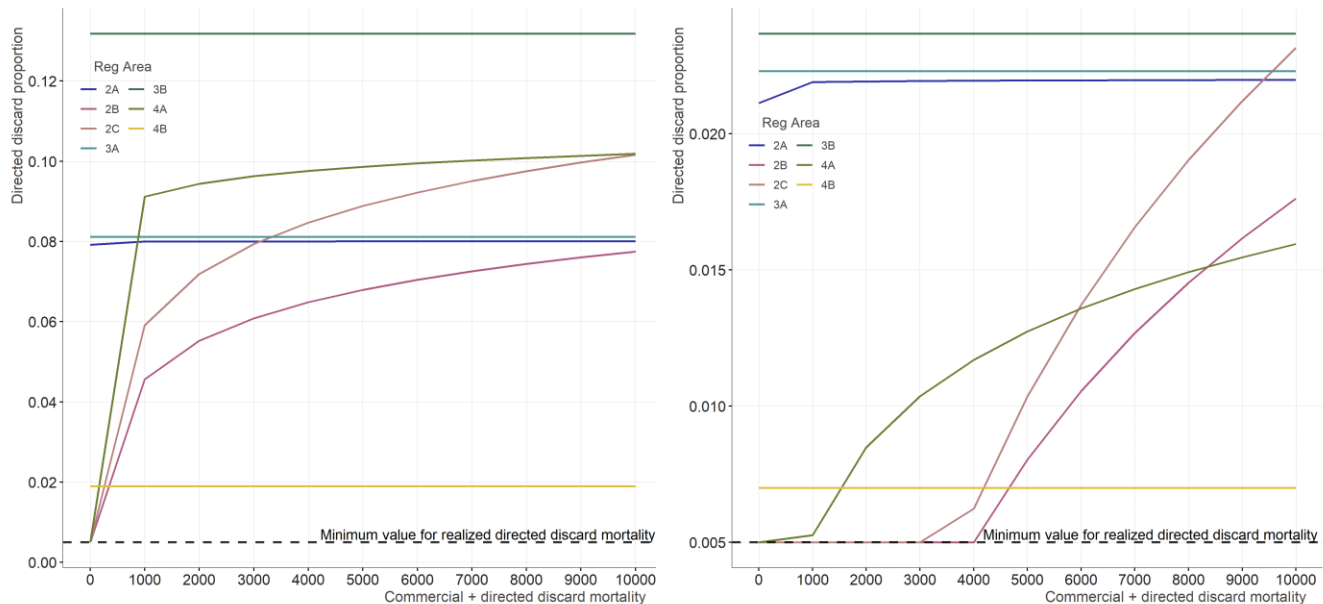
Figure 14. Proportion of directed discard mortality by IPHC Regulatory Area relative to different values of the commercial plus directed discard mortality with a male weight at age 8 equal to 4 lb (left) and 8 lb (right). The dashed line shows the 0.5% minimum.

Subsistence: subsistence mortality limits are set equal to the values observed in the previous year, except for IPHC Regulatory Area 2A, for which the subsistence value is set to 30,000 pounds (13.6 t). The realized subsistence mortality is randomly drawn from a lognormal distribution with a median equal to the limit subsistence mortality and a CV of 15%. The coastwide subsistence is then compared to the coastwide TCEY: if the allocation to the subsistence sector is higher than half of the overall TCEY, then the subsistence mortality in each regulatory area is adjusted so that the coastwide value will not exceed 50% of the coastwide TCEY.

Unguided recreational mortality: unguided recreational mortality is relevant only for IPHC Regulatory Areas 2C and 3A and it is randomly drawn from a lognormal distribution with a median equal to an average historical value (1.257 Mlb or 570 t for 2C and 1.579 Mlb or 716 t for 3A) and a 5% CV.

Recreational mortality: recreational mortality follows the catch sharing plans (CSPs) for IPHC Regulatory Areas in Region 2 and IPHC Regulatory Area 3A, noting that guided recreational mortality limits are only under the CSP in IPHC Regulatory Areas 2C and 3A and the total recreational mortality is the sum of guided and unguided. In IPHC Regulatory Areas 3B, 4A, 4B, and 4CDE, recreational mortality is included with subsistence because almost negligible.

Commercial mortality: is the remainder of the total mortality after subtracting all other sources of mortality.

Figure 15 and Figure 16 illustrate the results of the allocation procedure for each IPHC Regulatory Area when non-directed commercial discard mortality and unguided recreational are held constant at an average value. The

recreational and subsistence allocations for IPHC Regulatory Areas 4A and 4CDE are fixed at low values and aggregated to Biological Region in the OM. For this reason, these two sectors are not shown in Figure 16.
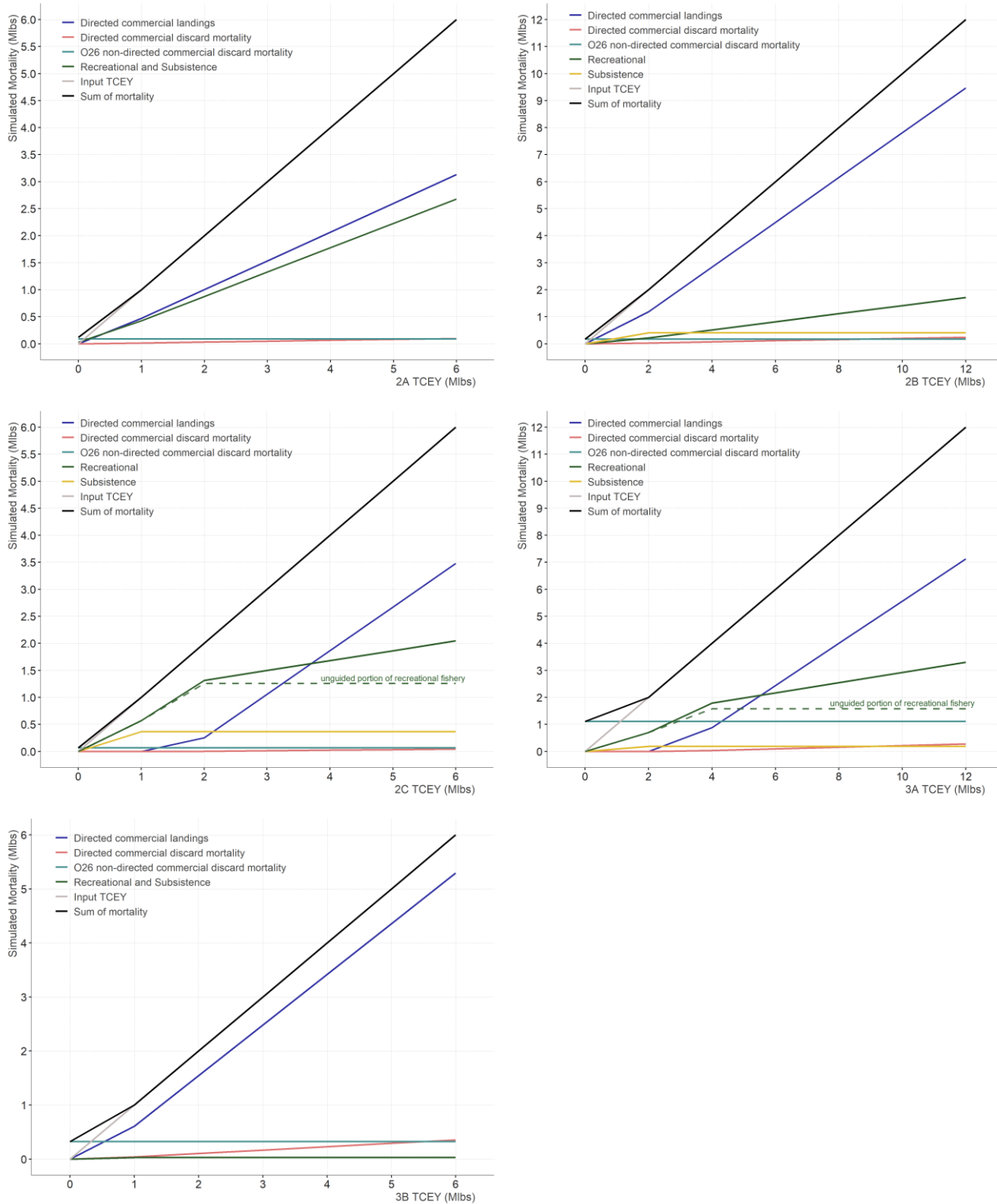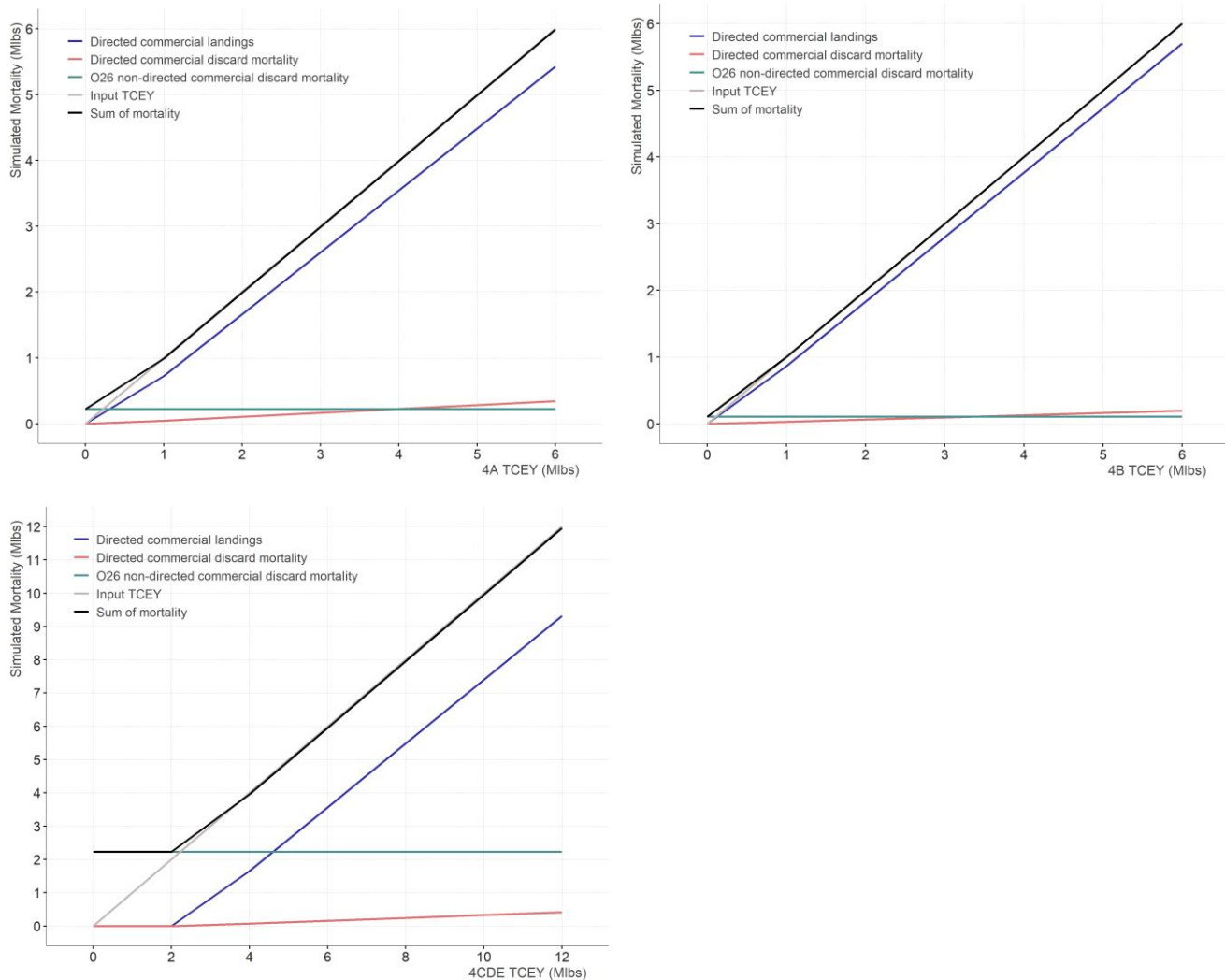

Figure 15. Allocation of the TCEY to sectors for IPHC Regulatory Areas 2A (top left) to 3B (bottom left) when O26 non-directed commercial discard mortality and unguided recreational are is assumed constant at average values. The input TCEY provided to the allocation function is shown in light gray, while the sum of mortalities after allocation is shown in black.

Figure 16. Allocation of the TCEY to sectors for IPHC Regulatory Areas 4A (top left), 4B (top right), and 4CDE (lower left) when O26 non-directed commercial discard mortality is assumed constant at an average value. The input TCEY provided to the allocation function is shown in light gray, while the sum of mortalities after allocation is shown in black.

3.3.2 Modelling length-at-age

The variability of length within an age group was modelled using Gaussian probability distributions with males and females modelled separately (Figure 17). The data used to inform the model are the length-at-age distributions converted from mean weight-at-age observations from the specific year, Biological Region, and sector. The CV of length-at-age for females and males was 0.16 and 0.11, respectively, determined from FISS observations. Length-weight parameters, by IPHC Regulatory Area, were taken from IPHC-2023-AM099-inf04. The proportion of fish in each age class above 32 inches was used to determine the probability of a fish being greater than 32 inches (O32) for each age (Figure 18).
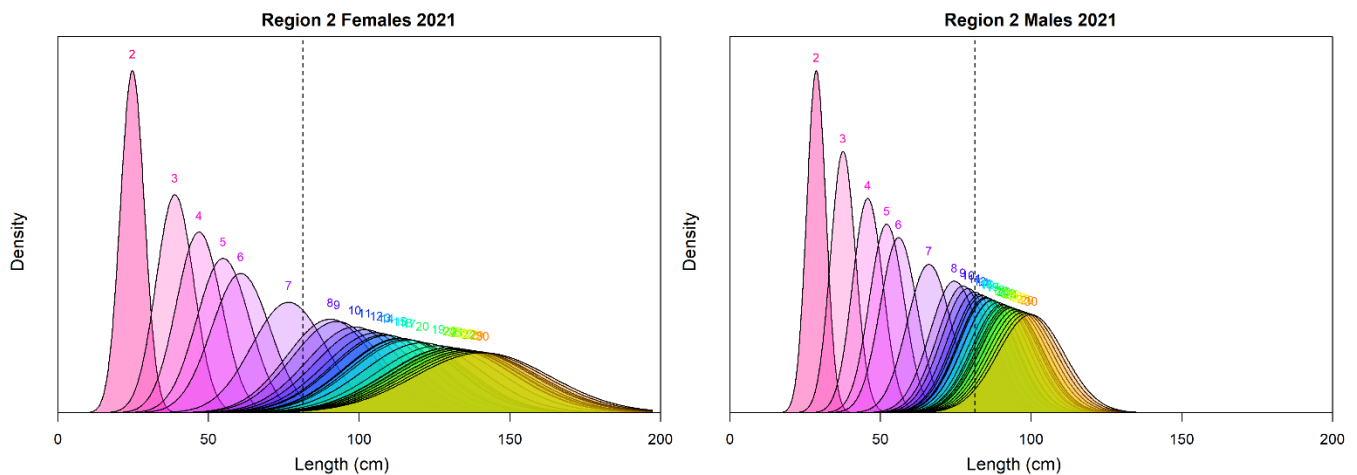
Region 2 Females 2021 Region 2 Males 2021

Figure 17: Length distribution at ages 2 to 30 for female (left) and male (right) Pacific halibut using mean weight-at-age in Region 2 and 2021 from directed commercial fisheries. The current size limit of 32 inches (81.3 cm) is shown as a dashed vertical line.
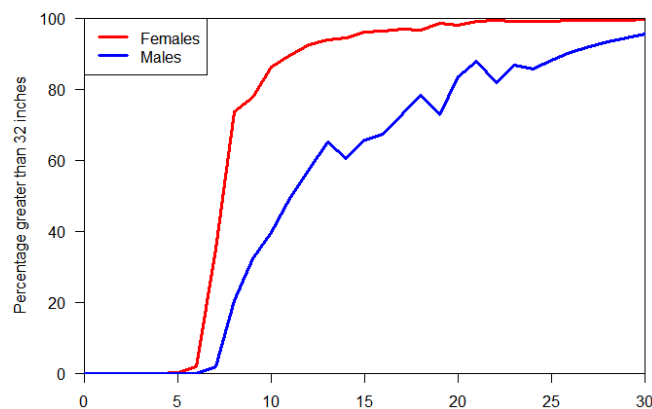

Figure 18: Percentage of fish above 32 inches by sex, calculated from mean weight-at-age observed in 2021 from the directed commercial fisheries in Biological Region 2.

3.3.3   Estimation procedure

The Estimation Model (EM) is analogous to the stock assessment and is how estimation error is included in the simulation. Using the data generated, it produces an annual estimate of stock size and stock status (measured as dynamic relative spawning biomass, RSB, and calculated as the current spawning biomass divided by unfished dynamic spawning biomass B_0) and provides the outputs for determination of the mortality limits for the next time step. Two methods were investigated for mimicking the estimation procedures to determine a coastwide total mortality limit and stock status (i.e. an estimation error approach and an estimation model approach). No estimation error can also used to allow for the examination of the effects of estimation error.

Estimation error approach

The OM can determine a total mortality (TM) consistent with an input fishing intensity (i.e. Spawning Potential Ratio, SPR) that may be modified at low stock status in the harvest control rule. This would be akin to no

estimation error, but in reality, both of these two components (TM and stock status) depend on estimates of stock biomass provided by the stock assessment model and are not known exactly.

The 2018 stock assessment ensemble was used to determine a reasonable amount of variability in these two components and the correlation between them (see Section 4.2.2 in IPHC-2018-SRB012-08). A 15% CV was deemed appropriate to cover both within- and between-model uncertainty for both total mortality and stock status. Correlated deviates ϵ for TM and stock status are sampled from a bivariate normal distribution with a correlation coefficient set at 0.5. Autocorrelation is implemented by independently applying it to the deviation of the estimated stock status and the estimated total mortality as follows

$$\left(\hat{X}_t - X_t\right) = \rho\left(\hat{X}_{t-1} - X_{t-1}\right) + \left(\sqrt{1 - \rho^2}\right)\epsilon_x \tag{49}$$

where $\hat{X}_t - X_t$ and $\hat{X}_{t-1} - X_{t-1}$ are the deviations for the quantity of interest (TM or stock status) in time step t and time step $t-1$ respectively, ρ is the autocorrelation parameter, and ϵ are the correlated zero-centered deviates for TM and stock status. The autocorrelation parameter was set at 0.4.

This method speeds up simulations while providing a reasonable approximation of the assessment process. Additionally, it may be used to test the effects of different levels of or bias in estimation error.

Estimation model approach

The estimation model is a simplified version of the actual stock assessment model incorporating the data generated with error from the OM. The EM estimates management quantities to mimic the stock assessment ensemble currently used for Pacific halibut. This approach is the recommended approach because it captures the correlated error and potential biases in the estimated management quantities, however it is much more computationally intensive than the estimation error approach and runs the risk that the fitting procedures may not find the optimal solution.

The coastwide model was chosen from the four models currently used in the stock assessment ensemble and was streamlined to increase efficiency and to reduce the time of the MSE simulations, yet retain part of the complexity and uncertainty captured by the full stock assessment ensemble. Using only one model may not capture the uncertainty that the stock assessment estimates, and may introduce bias that is countered by other models in the ensemble (Stewart & Hicks, 2018). However, running all models in an ensemble would be very time-consuming.

The streamlining of the coastwide models consisted of:

- Reducing the amount of data included (e.g. fewer years with age composition, long coastwide model starting from 1935, etc.)

- Using the optimized version of stock Synthesis (SS 3.30.13)

- Fixing annual deviations in selectivity parameters for the historical time series, and estimate only the deviations for the most recent 10 years.

- Using the ss.par file from the previous simulated EM for the starting parameters values in the next year's EM.

To speed up the estimation time, the hessian is not estimated, the estimation of parameters start after the last phase (so all parameters are estimated at the same time), the convergence criteria is relaxed, and screen outputs are reduced to a minimum.

Ten simulations with 60 year projections were run to evaluate the performance of the long coastwide stock synthesis assessment as estimation model with different OMs. The stock synthesis estimation model closely matches the stock status and the fishing intensity from the operating model (Figure 19).
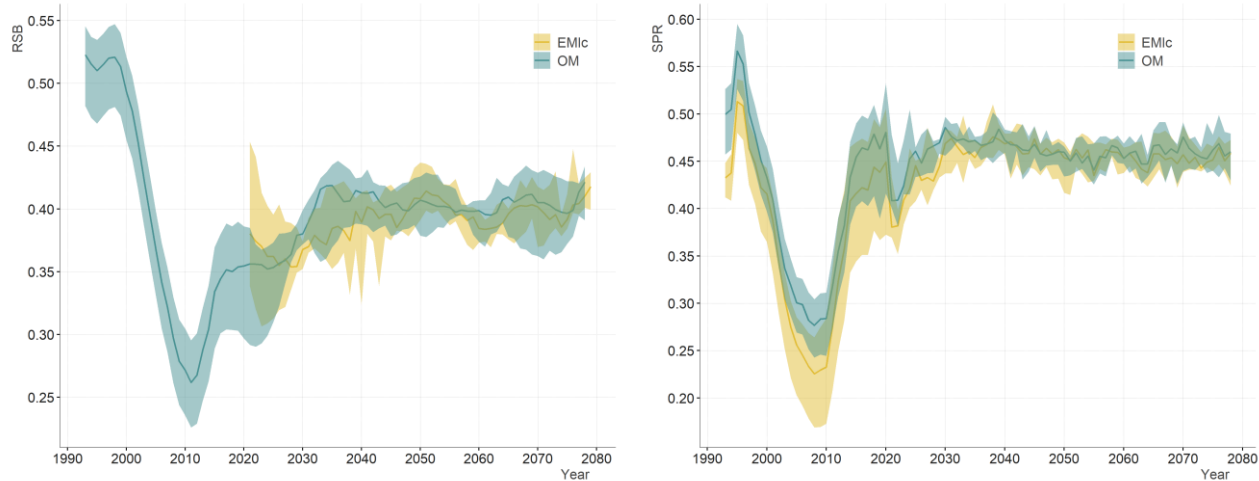

Figure 19: RSB (left) and SPR (right) as estimated by the OM (blue) and the long coastwide estimation model (yellow) for 10 simulations.

One year of forecast is performed to estimate the mortality associated with the target value of fishing intensity and the estimated stock status is used in the harvest control rule to determine whether fishing intensity is to be reduced. If that is the case, the forecast procedure is re-run with the new target fishing intensity and the updated corresponding total mortality is used.

A simplified short coastwide estimation model is currently being developed for incorporation as a second EM in the simulations to better represent the ensemble stock assessment. Until this is done, this estimation model approach is not complete and does not accurately represent the ensemble stock assessment. Therefore, it is not currently used.

3.3.4   Harvest rule

The harvest rule is the defined procedure that uses outputs from data generation and the estimation models to determine mortality limits for each fishery. Currently, this uses a fishing mortality rate based on SPR, a control rule to reduce the fishing intensity below specified stock sizes, a size limit of 32 inches for the directed commercial fisheries, and a distribution procedure to distribute the coastwide TCEY to each IPHC Regulatory Area and then to each fishery with an IPHC Regulatory Area. Different specifications of the harvest rule are the main focus for investigation of management procedures for Pacific halibut. SPR and distribution procedures have been evaluated in the past (IPHC-2021-AM097-11). Size limits and not conducting annual stock assessments (multi-year assessments) have also been investigated (IPHC-2023-AM099-13).

Harvest rules and distribution procedures are coded in R as individual functions and are called within the framework once stock status and TM are determined by the estimation model.

3.4 Simulation and Evaluation

3.4.1 Processes and parameters

There are many processes with various parameters that make up the OM including population, fishery, and environmental parameters. Some of the parameters are simply an input parameter that drives the population (called input parameters). Derived parameters are calculated from parameters, inputs, and outputs. For example, natural mortality (M) is an input parameter that in combination with other parameters results in a calculated spawning biomass (a derived parameter). Various processes and associated parameters are described below, and it is noted where some processes are simulated differently in projections. A description of how uncertainty is incorporated is provided first.

3.4.1.1 *Incorporating uncertainty in the simulated trajectories*

Uncertainty is important to consider, as the goal of an MSE is to develop management procedures that are robust to uncertainty. The OM should simulate potential states of the population in the future, uncertainties within the management procedure, and variability when implementing the management procedure.

The conditioned OM is a representation of the Pacific halibut population and matches observations from the fishery, survey, and research. Uncertainty in these observations is included in the OM by varying parameters described below. Parameters vary between simulated trajectories and are drawn from correlated probability distributions that are derived from the stock assessment models as well as estimated parameters when conditioning the OM. These sets of parameters result in multiple historical population trajectories from which to begin the projections. The major sources of uncertainty in the OM are described in Table 7.

Table 7: Major sources of parameter uncertainty and variability in the conditioned operating model (OM).

Process	Uncertainty
Natural Mortality (M)	Variability determined from assessment
Steepness (h)	Variability from a diffuse normal prior bounded between 0.6 and 1 with a mean of 0.75
Average recruitment (R_0)	Effect of the coastwide environmental regime shift and variability determined from conditioning
Recruitment	Random lognormal deviations. Variability on distribution to Biological Regions determined from conditioning
Movement	Parameter uncertainty estimated during the conditioning process

Variability in the projected population is a result of initializing the population up to the current year with a range of parameters to recreate a range of historical trajectories and then include additional variability in certain population processes in the projection. The major sources of variability in the projections are shown in Table 8 and some are described in more detail below.

3.4.1.2 *Simulating regime shifts*

An environmental regime is used in the stock assessment to determine if average recruitment is high or low and to allow for different movement-at-age. These simulated environmental regime shifts may be used for other processes as needed. This is based on the Pacific Decadal Oscillation[1] (PDO, Figure 20) and the value is 0 or 1 depending on classified cool or warm years, respectively (Figure 21).

The regime was simulated in the MSE by randomly generating a 0 or 1 to indicate the regime in that future year. To encourage runs of a regime between 15 and 30 years (an assumption of the common periodicity, although

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[1] http://research.jisao.washington.edu/pdo/, Mantua et al. 1997

recent years have suggested less), the environmental index was simulated as a semi-Markov process, where the next year depends on the current year. However, the probability of changing to the opposite regime was a function of the length of the current regime with a probability of changing equal to 0.5 at 20 years, and a very high probability of changing at 40 years (Figure 22). The simulated length of a regime was most often between 20 and 30 years, with occasional runs between 5 and 20 years. Regimes were mixed for the projection lengths commonly simulated (Figure 23).

Table 8: Major sources of projected variability in the operating model (OM), not including parameter variability described in Table 7.

Process	Variability
Average recruitment (R_0)	Effect of the coastwide environmental regime shift, modelled as an autocorrelated indicator based on properties of the PDO
Steepness (h)	Variability from a normal prior bounded between 0.6 and 0.98 with a mean of 0.75 and a standard deviation (and correlations) determined from the Hessian of an assessment run with steepness estimated.
Recruitment	Random lognormal deviations
Movement	Variability on movement parameters determined from the conditioning process. Change in parameters synchronized with PDO regime shift
Size-at-age	Annual and cohort deviations in weight-at-age by Biological Region, with bounds, determined from historical observations
Sector mortality	Sector mortality allocation variability on non-directed commercial discard mortality, directed discard mortality, and unguided recreational mortality within an area

3.4.1.3   Recruitment

Coastwide spawning biomass determines coastwide recruitment which is distributed to each region based on specified parameters (i.e. proportions). These proportions sum to 1, thus n_R–1 proportions need to be supplied or estimated. The framework currently only allows for the proportions to vary with environmental regime. Therefore, the Pacific halibut OM currently estimates three proportions for Regions 2, 3, and 4 in each regime. The proportion for 4B within a regime is determined from those three proportions.

It is worth noting that movement probabilities-at-age (described below) are specified for young ages that are not well observed in many data sources and are not part of the spawning biomass. Therefore, the movement of these young ages and the proportion of recruitment in a region are confounded. A mis-specified proportion of age-0 fish in a region can be counter-balanced by movement of young fish into or out of that region.

The magnitude of recruitment is determined from the stock-recruit relationship with a steepness bounded between 0.6 and 0.98, the environmental relationship as described above, and a lognormal deviation with a standard deviation representing recruitment variability.
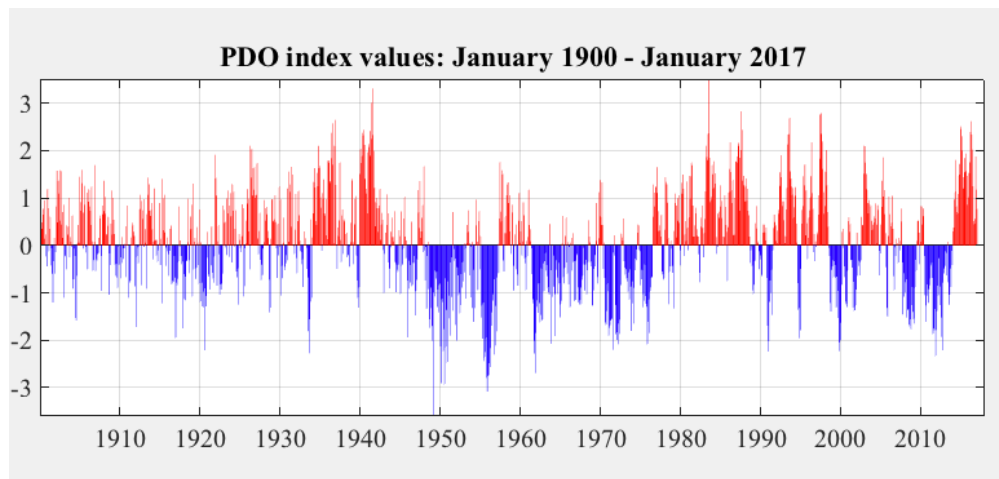
Figure 20: Pacific Decadal Oscillation (PDO) (figure from http://research.jisao.washington.edu/pdo/)
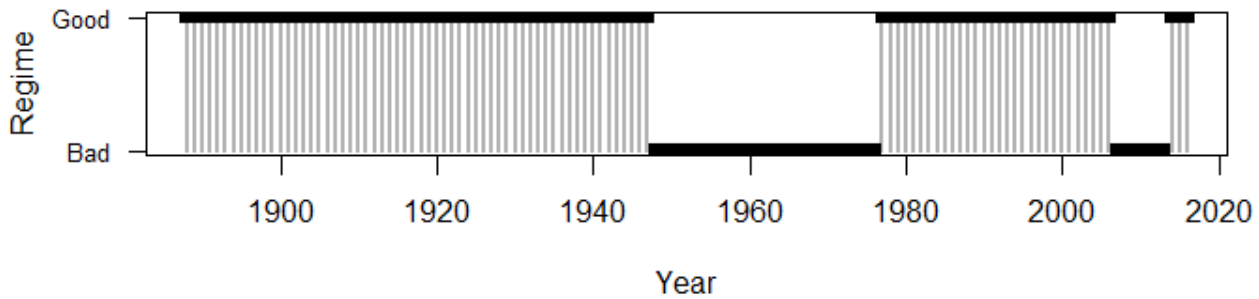

Figure 21: Good and bad regimes identified in the Pacific halibut stock assessment for 1888–2016 based on the Pacific Decadal Oscillation.
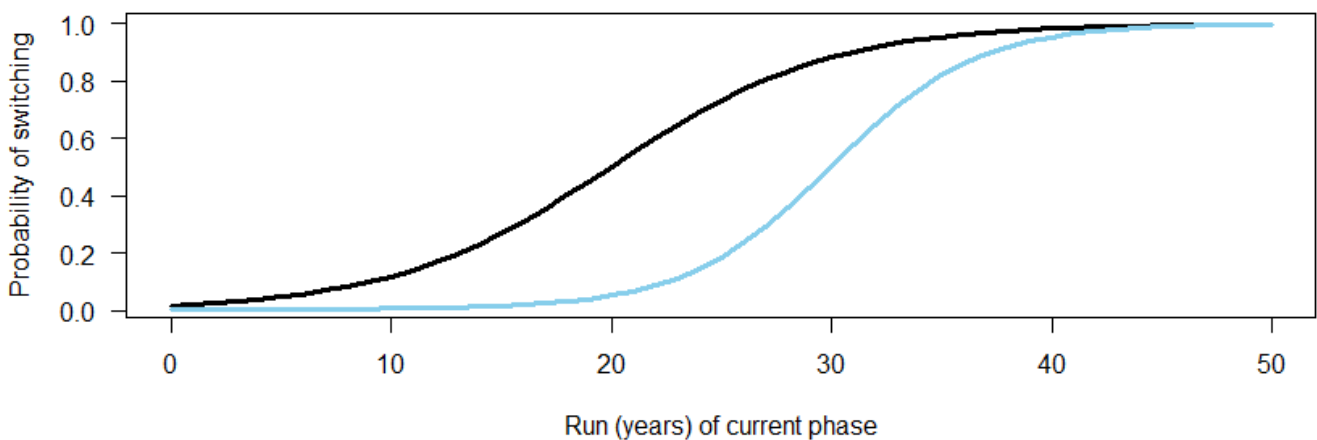

Figure 22. Modelled probability of the environmental regime switching to the opposite regime based on the number of years (run) of the current regime. The black line is the current parametrization and the blue line is a former parameterization.
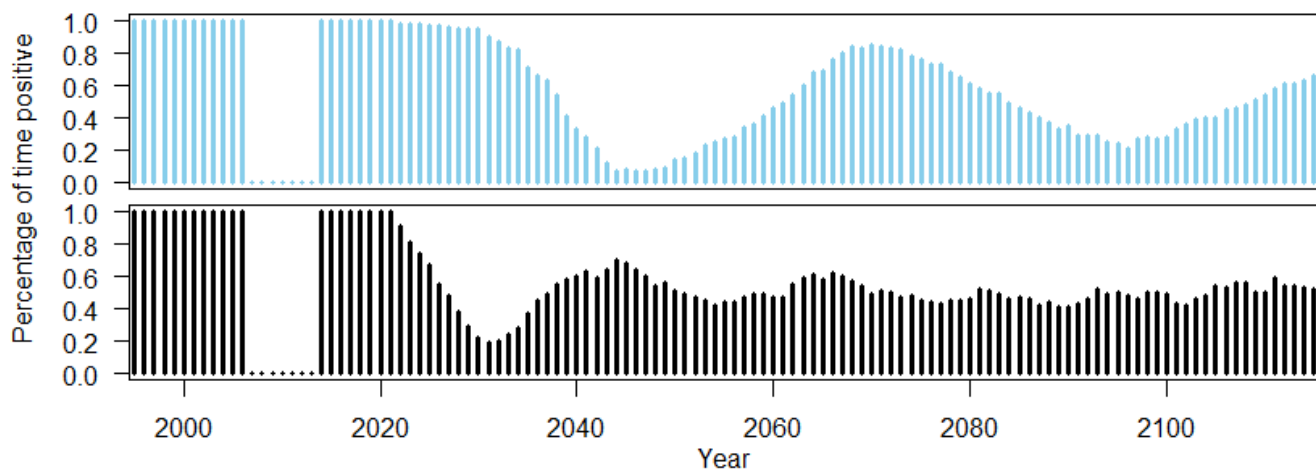
Figure 23. Percentage of simulations that the simulated PDO was positive for two parameterizations of the probability that the PDO switches. The top and bottom plots correspond to Figure 22. The top has a 0.5 probability of change at 30 years while the bottom plot is 20 years. The slope and y intercept of the logistic function is 0.3 and 0.005 in the top plot and 0.2 and 0.0 in the bottom plot.

3.4.1.4 *Movement*

Many data sources are available to inform Pacific halibut movement. Decades of tagging studies and observations have shown that inter-annual and intra-annual movement characterizes both the juvenile and adult stages and apply across all IPHC Regulatory Areas (Carpi, et al., 2021). The conceptual model of halibut ontogenetic and seasonal migration, including main spawning and nursery grounds, as per the most current knowledge, was used to assist in parameterizing movement rates in the OM.

In 2015, the many sources of information were assembled into a single framework representing the IPHC's best available information regarding movement-at-age among Biological Regions. Key assumptions in constructing this hypothesis included:

* ages 0–1 do not move (most of the young Pacific halibut reported in Hilborn et al (1995) were aged 2–4),

* movement generally increases from ages 2–4,

* age-2 Pacific halibut cannot move from Region 4 to Region 2 in a single year, and

* relative movement rates of Pacific halibut age 2–4 to/from Region 4 are similar to those observed for 2–4-year-old Pacific halibut compared to older Pacific halibut in Region 3.

Based on these assumptions, appreciable emigration is estimated to occur from Region 4, decreasing with age. Pacific halibut age-2 to age-4 move from Region 3 to Region 2 and from Region 4B to Regions 3 and 2, and some movement of older Pacific halibut is estimated to occur from Region 2 back to Region 3 (Figure 24).

The conceptual model and assembled movement rates were used to inform the development of the MSE operating model framework and is being used as a starting point to incorporate variability and alternative movement hypotheses in Pacific halibut movement dynamics. Movement in the OM is modelled using a transition matrix as the proportion of individuals that move from one Biological Region to another for each age class in each year.

The transition matrix with movement probabilities from one region to another (including staying in the region of origin) can either be entered directly or parameterized using several functional forms. Current functional forms include *constant*, *exponential*, and *two-sided exponential*, as shown in Equations (11) to (14), and can closely mimic the movement probabilities based on observations (described above), as seen in Figure 25.

The Pacific halibut OM uses these functional forms for different transition probabilities. Movement probabilities from 3 to 2 and 4 to 3 using the double exponential formulation were estimated during the conditioning process. Parameters for these movement probabilities were allowed to differ between environmental regimes resulting in the potential for two different movement curves for these two transitions. Other movement parameters were fixed to estimates from data (Figure 24) except that movement probabilities from 4 to 2, 2 to 4, 4B to 2, and 2 to 4B were set to zero for all ages. This makes the assumption that a Pacific halibut cannot travel between these non-adjacent areas in an annual time step even though significant probabilities of movement-at-age from 4 to 2 are predicted to occur from observations.
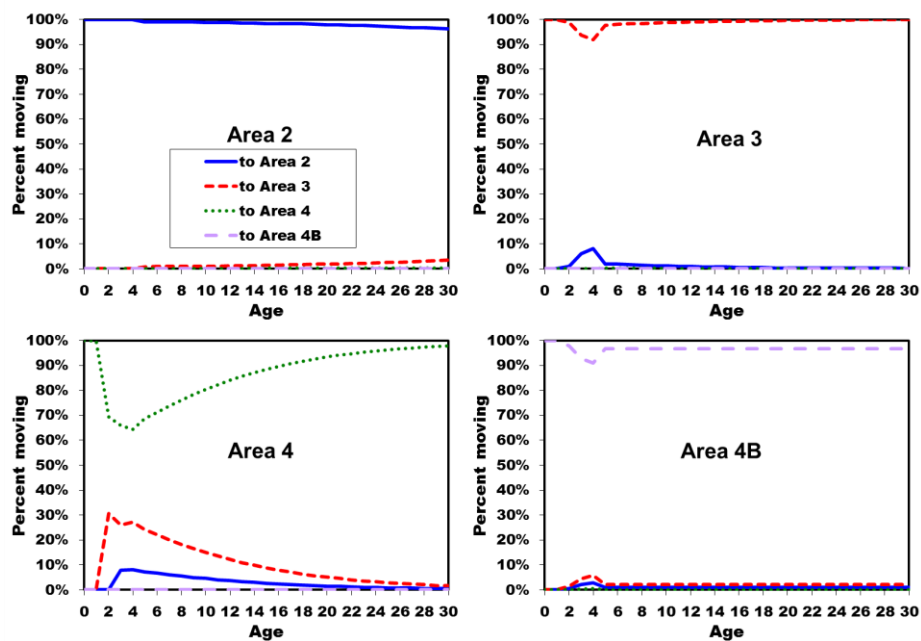

Figure 24: Estimated aggregate annual movement rates by age from Biological Regions (panels) based on currently available data (from IPHC-2019-AM095-08).
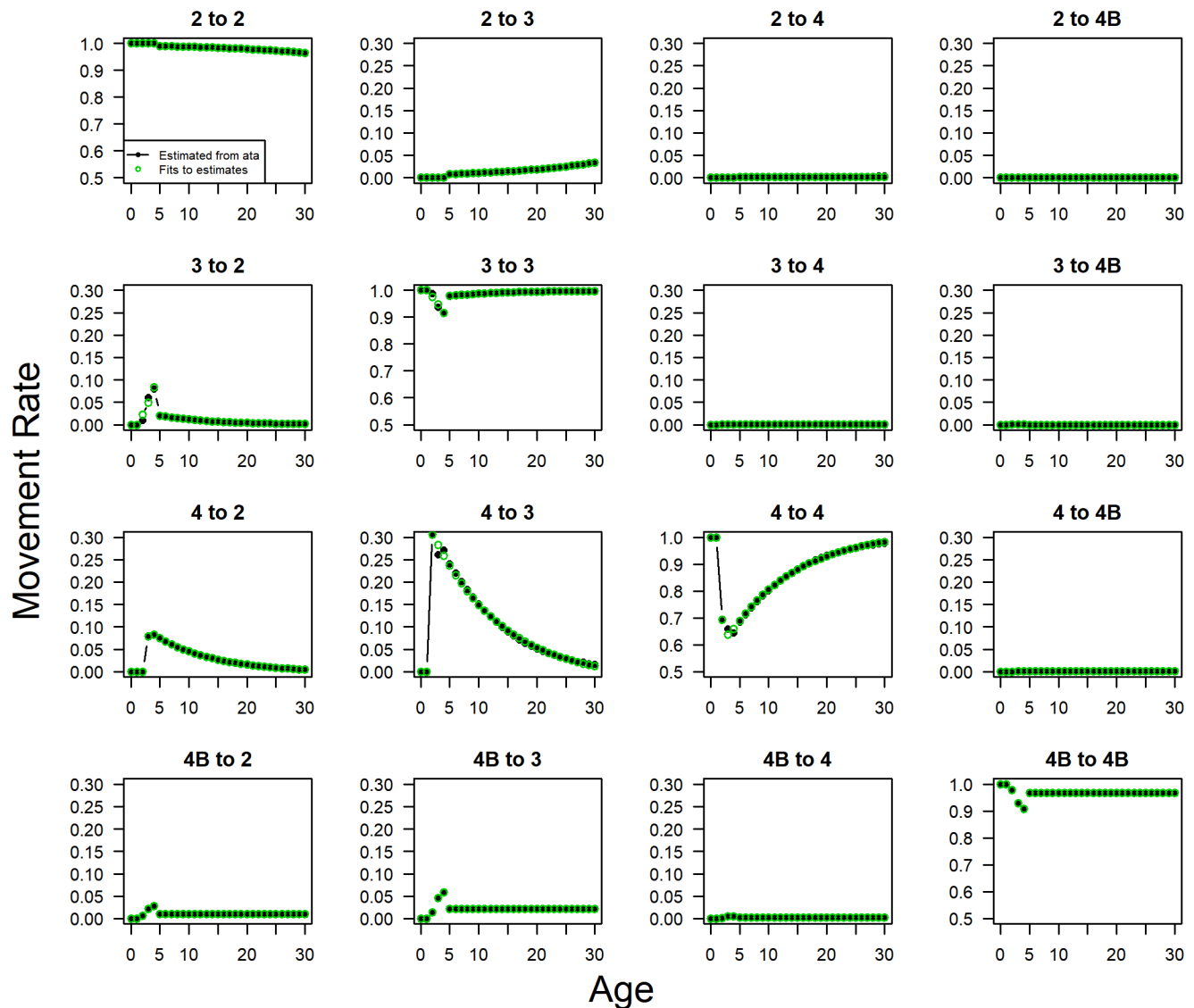
Figure 25: Estimates of movement rates by age from data (black solid circles) and fits (green circles) to those estimates using various functional forms described in Equations (11) to (14).

3.4.1.5 Fishery and survey selectivity and retention

Selectivity and retention determine the age composition of fishery mortality and ensure the removal of appropriate numbers-at-age from the population when mortality occurs in the annual time-step (see Section 2.3.4). Some fish that are not retained may survive; thus, a discard mortality rate (DMR) is used to indicate the proportion of fish that are not retained and die after release. Historical retained mortality (i.e. landings) is modelled in the sector called "directed commercial" and historical mortality from fish released at sea are modelled in the sector called "directed commercial discard mortality" and is entered directly from estimates. Therefore, a retention curve and DMR are not needed for the historical specifications. However, there is the option to model retention (and thus discards) which is used in projections to investigate the effect of various management procedures on discard mortality (such as size limits).

Parameters for selectivity were determined from the 2022 stock assessment (IPHC-2023-SA-01), including annual deviations in selectivity for the directed fisheries and the survey. Selectivity for the directed commercial

and survey fisheries were made asymptotic because movement should account for at least some of the differences in availability between Biological Regions.

Retention-at-age, combined with selectivity-at-age, can separate landings and discards in the OM. However, selectivity in this context encompasses discarded and retained fish, which is not determined in the stock assessment. Fortunately, landings are the product of selectivity-at-age and retention-at-age, which is called 'keep-at-age' here, and the directed commercial fisheries model only landings, thus use keep-at-age. Dividing keep-at-age (from directed commercial fleets) by retention-at-age (from length-at-age distributions and length-weight relationships) determines selectivity-at-age for a fleet that models retention (landings) and discards. O32 discards are a small component of the directed commercial fleet that can be accounted for by reducing the asymptote of the retention curve.

The above method was used to determine selectivity and retention curves for new fleets in the OM (projections only) that replaces the historical directed commercial and discard fleets, modelling them as one and accounting for any size limit. The keep curve at young ages was sensitive to small values of retention, and the resulting keep curve was often unrealistically jagged. Therefore the following assumptions were enforced:

- Retention was forced to be zero at ages 5 and under to avoid spikes in selectivity at young ages.

- The retention curve was parameterized to a double logistic formulation before calculating selectivity to smooth it and prepare it for use in the OM.

- The selectivity was parameterized as an asymptotic double normal to smooth the curve and prepare it for use in the OM.

All the curves in this process are shown in Figure 26 for 2021, determined from the 2021 stock assessment and previous operating models.

To ground-truth this method and determine if any adjustments should be made to the calculated selectivity, the U32 discards were predicted in the OM for the directed commercial fleets in each IPHC Regulatory Area for the years 2010 to 2021, and the peak parameter was adjusted until the predicted discards matched the observed U32 discards. This was done individually for each year because misfitting the discards in one year changes the dynamics in subsequent years. It was also performed separately for each OM model. Only one parameter could be chosen for the adjustment because only one observation is being fitted. The ascending limb was not fit, although estimated ascending limb deviations from the stock assessment are more correlated with weight-at-age than peak devations. However, the peak parameter may be a good choice since the temporal variability in size-at-age is generally consistent across younger age classes.

The adjustment to the peak parameter of the asymptotic double normal selectivity curve differed for each IPHC Regulatory Area and ranged from an adjustment of near 8 years younger to an adjustment of near 4 years older, depending on the year and area (Figure 27). The adjustments for each OM model (2022 OM) were similar. Even though the years differed substantially, the general patterns were similar within a Biological Region and are intuitive. First, there was a general trend of shifting selectivity to younger ages. Additionally, IPHC Biological Region 3 often sees a lot of undersized Pacific halibut, and the adjustment was towards the youngest fish in both IPHC Regulatory Areas 3A and 3B. This may be because the fishery is unable to avoid these small fish as well as in other IPHC Regulatory Areas. The range of adjustments in each IPHC Regulatory Areas could be natural variability as well as a result of uncertainty in the discards entered into the model.
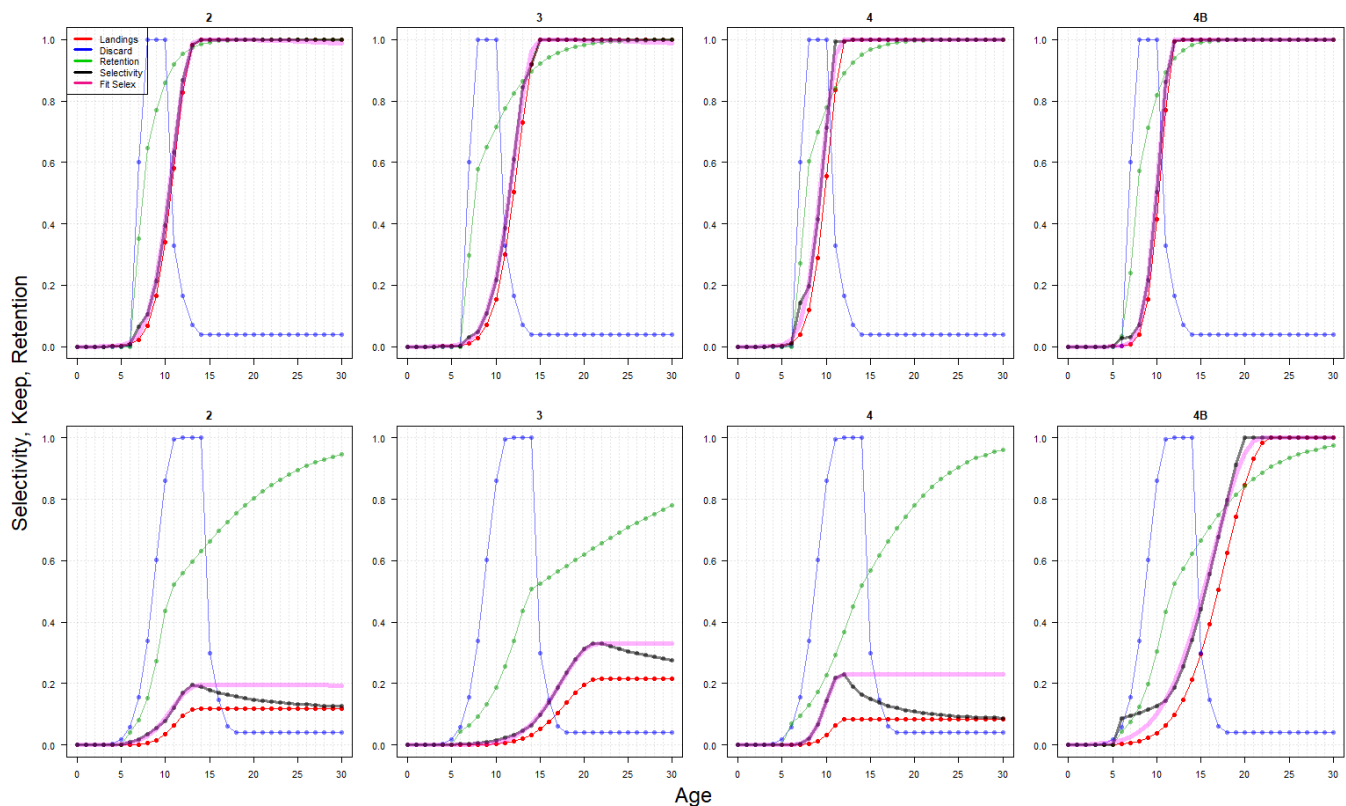
Figure 26. Selectivity, retention, and keep curves for each Biological Region (columns) and sex (rows, females in the top panels, males on the bottom panels) calculated using values from 2021 in the 2021 stock assessment (IPHC-2022-SA-01). Landings is the keep curve for the directed commercial fleet as entered in the OM (red curve with dots). Discard (blue) is the selectivity curve for directed discard mortality as entered in the OM. Retention (green) is the double logistic parameterization of the retention calculated from weight-at-age, length-at-weight, and length-at-age relationships. Selectivity (black) is the selectivity-at-age determined from keep and retention. The selectivity curve fitted to selectivity using a asymptotic double normal parameterization is shown in pink.

Similarly, an adjustment to the asymptote of the retention curve was estimated using O32 discards (using a grid approach over specific values to save time). This adjustment ranged from near 0 to a deviate slightly more than 0.05 applied to lower the asymptote. Triangle distributions were roughly fit to the estimated adjustments, as shown in Figure 28, and were the same for each OM model. The deviation to the retention asymptote were sampled from these triangle distributions.

This method was used to parameterize a directed commercial retention fleet in the OM for each IPHC Regulatory Area. Eight additional fleets, duplicating the directed commercial and directed discard fleets, were added to each OM model and parameterized with selectivity and retention using the methods above. The median values for each OM model and IPHC Regulatory Area from the ground-truthing exercise (Figure 27) were used to determine the base selectivity for these directed commercial retention fleets. The projections, starting in 2022, assigned directed commercial fishing retained mortality to these fleets and zero fishing mortality was assigned to the original directed commercial and directed discard fleets. Directed commercial discards are therefore a result of the OM and not directly needed as an input. This allows for the MP to account for directed commercial discards using the methods currently in practice, whereas realized directed commercial discards may differ from what was assumed when setting mortality limits. The greatest benefit of this formulation is that any size limit can be consistently evaluated, and appropriately linked to changing weight-at-age.

A benefit of modelling landings and discards separately is that separate mean weight-at-age vectors can be used for each mortality type, effectively accounting for potentially smaller sized fish at each age being discarded. This benefit was maintained in the OM directed commercial retention fleets by allowing for different mean weight-at-age vectors in the kept and discard components of the fishing mortality.

When projecting the population and fisheries, mean weight-at-age is dynamic, thus the retention and selectivity curves must be recalculated based on current mean weight-at-age. The stock assessment applies annual deviations to the peak and ascending limb parameters of selectivity to account for temporal changes in mean weight-at-age; the annual recalculation of retention and selectivity mimics this process.
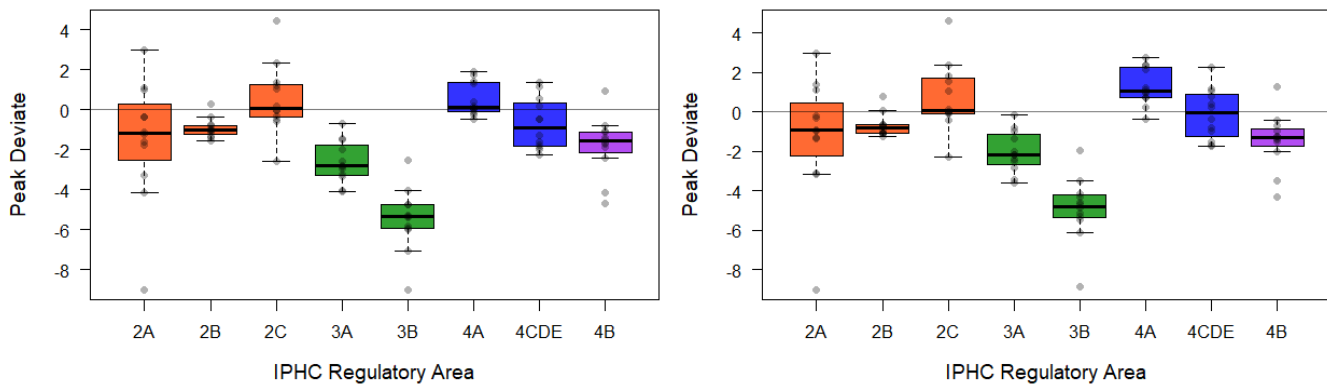

Figure 27. Estimated deviations (in age) from the peak parameter for selectivity for the medAAF (left) and medCW (right) OM models and IPHC Regulatory Area across the years 2010 to 2021. Colors are associated with each Biological Region. Dots indicate each individual year.
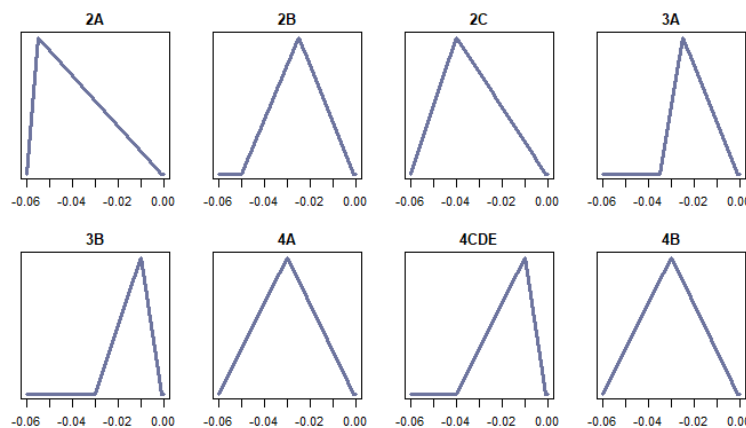

Figure 28. Triangle distributions used to draw random deviates for the retention asymptote. The distributions are the same for each OM model.

3.4.1.6 *Maturity and spawning output*

Spawning biomass for Pacific halibut is currently calculated from a maturity-at-age ogive that is assumed to be constant over years. There is currently no evidence (IPHC-2020-SA-02) for skip spawning or maternal effects (increased reproductive output or offspring survival for larger/older females) and they are not modelled, but could be added. The 2017 stock assessment (IPHC-2018-AM094-10) examined the sensitivity to a trend in declining spawning potential (caused by a shift in maturity or increased skip spawning) and found that under

that condition there was a bias in both scale and trend of recent estimated spawning biomass. Ongoing research on maturity and skip spawning will help to inform future implementations of the basis for variability in the determination of spawning output.

For now, maturity is parameterized as it is in the 2022 stock assessment for Pacific halibut (IPHC-2023-SA-01) with a single maturity curve for all years (Figure 29). The age at 50% mature occurs at slightly less than 12 years.
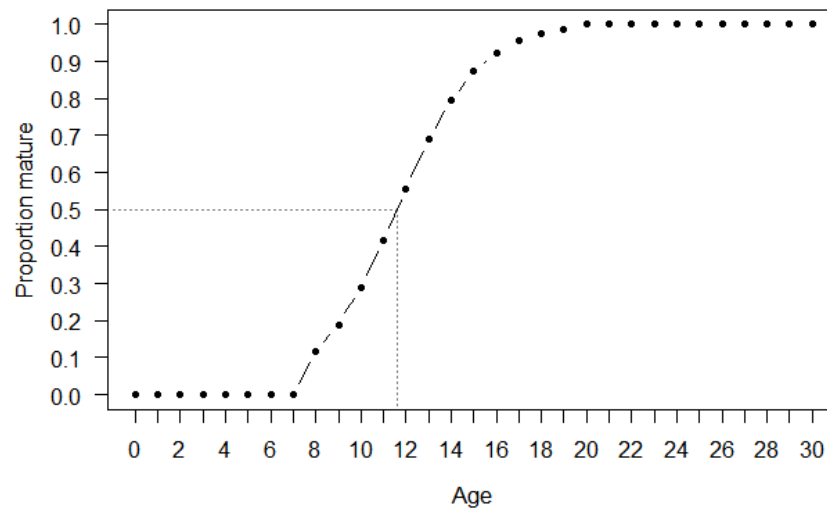

Figure 29: Proportion mature-at-age specified in the Pacific halibut operating model.

3.4.1.7 *Weight-at-age*

Empirical weight-at-age by region for the population, fisheries, and survey for the historical period are determined using observations from the FISS and the fisheries, as is done with the stock assessment models (IPHC-2023-SA-02). Smoothed observations of weight-at-age from NMFS trawl surveys were used to augment ages 1–7 fishery and survey weights-at-age. Population weight-at-age is smoothed across years to reduce observation error. Finally, survey and population weight-at-age prior to 1997 is scaled to fishery data because survey observations are limited if present at all.

Weight-at-age varies over time historically, and the projections capture that variation using a random walk from the previous year. It is important to simulate time-varying weight-at-age because it is an influential contributor to the yield and scale of the Pacific halibut stock. This variability was implemented using randomly generated deviates that are linked to weight-at-age across all ages and regions, as well as deviates linked to each age within a region. This results a similar coastwide trend in weight-at-age, while allowing for some regional and age-specific variability.

The method used to simulate weight-at-age is as follows.

A single deviate (d_1) is generated from a normal distribution with a standard deviation determined from a 5% coefficient of variation and the mean of the weight-at-age from 1935 to 2019.

A deviate for each age 6 and greater, sex, region, and fishery ($d_{2,a,s,r,f}$) is generated from a normal distribution with a standard deviation determined from a 1% coefficient of variation and the mean of the weight-at-age from 1935 to 2019.

The projected weight-at-age for a region/fishery is from an ARIMA process with deviates d_1 and $d_{2,a,s,r,f}$ applied

$$w_{a,s,r,f} = w_{a-1,s,r,f} + 0.45\big(w_{a-1,s,r,f} - w_{a-2,s,r,f}\big)$$
$$+ 0.30\big(w_{a-1,s,r,f} - w_{a-2,s,r,f}\big) + d_1 + d_{2,a,s,r,f} \tag{50}$$

where 0.45 and 0.30 were determined by fitting an ARIMA(2,1,0) model to past observations of weight-at-age. The CVs for d_1 and d_2 were determined from past variability and ad hoc matching of simulated projection outputs to past variability.

Projected weight-at-age was maintained within bounds determined by extending the observed range of historical weight-at-age by 5%. If a weight at a specific age exceeded the bound, the deviation for that weight-at-age was reduced such that it was at the bound.

The overall deviate d_1 above is the main driver of weight-at-age and captures the past observations of variability in weight-at-age over time. Example projections are shown in Figure 30.
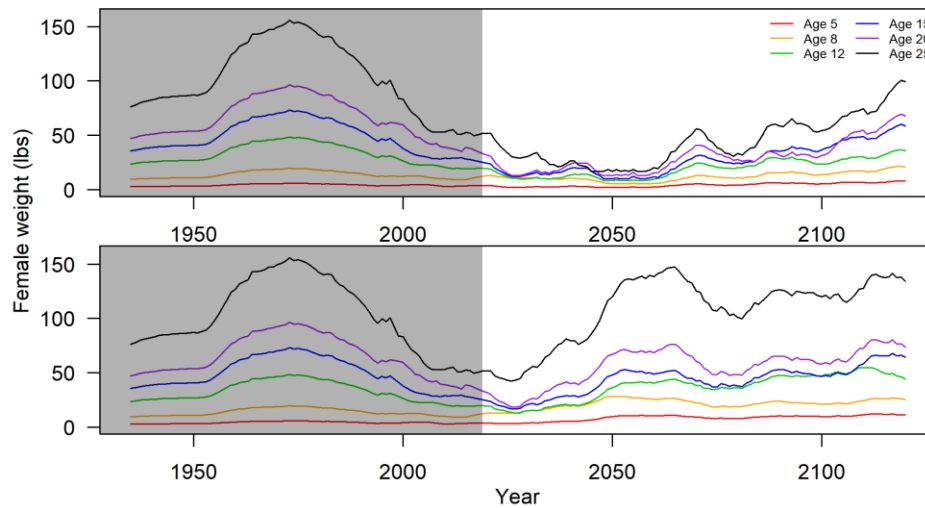

Figure 30: Past observed (shaded area) and two examples of possible one-hundred-year projections of weight at ages 5, 8, 12, 15, 20, and 25.

3.4.2 Conditioning the Pacific Halibut operating model

Conditioning the OM is the process of estimating/defining parameters to create a population model that best describes the current understanding of that population. That may involve fitting parameters to data, determining parameters from external analysis, or specifying parameters based on an understanding of the process and its variability. General descriptions of various observations and data that are used in the conditioning of the operating model are given below. Some of these observations are described in more detail in Section 3.4.1.

The MSE Operating Model (OM) was updated in 2023 based on assumptions and outputs of the 2022 full stock assessment (IPHC-2023-SA-01) and the data available at the end of 2022 (IPHC-2023-SA-02). The OM is an age-structured population dynamics model with movement between four Biological Regions. Multiple fishing sectors are modelled within IPHC Regulatory Areas along with landings and discard mortality. The OM incorporates four individual models (OM1–OM4) and integrates them into an ensemble to account for structural uncertainty and differing hypotheses about recruitment and distribution.

The OM was developed as a simulation model to explore alternate hypotheses of the population and is parameterized to allow for the specification of alternative hypotheses. However, this introduces the possibility of overparameterization and confounding between parameters. For example, movement between regions and the proportion of recruitment to each region are confounded and not easily separated with the inputs being conditioned to. Therefore, assumptions and priors are used to aid the conditioning process.

The early portion of the time-series of observations (1888–1957) is challenging to model due to relatively little data, some significant catches in Biological Region 2, and the potential for unknown differences in population dynamics (e.g. movement between Biological Regions) compared to recent periods. To reduce the technical complexity and focus on information contained in the richer data set in the later period, the 2023 OM individual models were started in 1958. In order to allow for flexible starting conditions, 30 years of initial recruitment and an average fishing mortality were estimated for each fleet. This initialized the models after a bottleneck of potentially high fishing mortality in the 1930's that is confounded with the estimation of movement, yet allowed for a sufficient period of time to burn-in the population such that projections began with at an appropriate state. The period from 1958 to the present includes major changes in fishery catches, weight-at-age in the population, and population size.

Fishing mortality

The mortality of Pacific halibut due to fishing (i.e., landings and discard mortality) are not treated as data in the stock assessment or OM because they are entered as fixed, known values without error (empirical observations). Fishing mortality is a very important driver of the population dynamics.

FISS modelled indices

These data are an annual relative index of abundance or biomass. They represent changes in abundance or biomass from year to year, but do not represent the absolute scale. Fishery-Independent Setline Survey (FISS) numbers-per-unit-effort (NPUE), survey weight-per-unit-effort (WPUE), and fishery catch-per-unit-effort in weight (CPUE) are available for Pacific halibut. The survey index in numbers-per-unit-effort (NPUE) is available coastwide, by Biological Region, or by IPHC Regulatory Area.

FISS age compositions

These data are the numbers-at-age of Pacific halibut (commonly in proportions) in the survey catches and fishery catches. Survey observations are available for each sex. Differences in sex ratios inform differences in selectivity, availability, and potentially movement between areas.

FISS modelled stock distribution

The stock distribution estimated from modelled FISS data are available by IPHC Regulatory Area and by Biological Region. Changes in this distribution over time may indicate differences in fishing pressure between areas and may also inform movement.

Weight-at-age

These data are the weight-at-age of Pacific halibut observed from various sources and are commonly summarized as the average weight-at-age. They are entered as empirical data in the stock assessment and are not involved in the fitting process.

Environmental observations

The Pacific halibut stock assessment uses an index linked to average recruitment (high or low) that is developed from the Pacific Decadal Oscillation (PDO). Additional environmental observations may be useful to condition the multi-area operating model. These may be ocean temperatures or prey abundance, for example.

Predictions from the stock assessment

The stock assessment integrates various data sources to estimate population quantities as well as uncertainty in those quantities. Four individual models are combined in an ensemble to account for structural and parameter uncertainty. Two of the individual models incorporate a short time-series starting in 1993, thus only estimates from 1993 onward can be supplied by the ensemble of four models, while estimates from 1888 to present are supplied by an ensemble of the two 'long' models. Each 'short' and 'long' model uses either coastwide fishing fleets or an areas-as-fleets approach with fishing fleets defined by Biological Regions. Individual OM models were conditioned to either the coastwide models or the areas-as fleets models.

The observations described above are used during conditioning to determine estimates of various parameters that best reproduce the observations. Uncertainty in these parameters is determined based on statistical theory and used to introduce variability into the population. The conditioning process is described next.

3.4.2.1   Parameters and likelihoods

Parameters for R_0, a multiplier on initial fishing mortality, proportion of recruitment to each Biological Region for each environmental regime, and movement from 3 to 2, and 4 to 3 for each environmental regime were estimated by minimizing an objective function based on the weighted sum of lognormal likelihoods for spawning biomass predictions and region-specific modelled survey indices, robustified multivariate normal likelihoods for the proportion of survey biomass in each region, and observed proportions at age from the FISS. Other parameters were fixed at values estimated in the 2022 stock assessment (IPHC-2023-SA-01) or from external analyses, as noted above and in Table 9. For example, natural mortality was fixed separately for males and females, maturity, mean weight-at-age, recruitment deviations, the relationship between R_0 and the Pacific Decadal Oscillation (PDO), selectivity, and fishing mortality were fixed at the values from the stock assessment. The parameters estimated are listed in Table 10.

Table 9. Parameters and the assessment model spawning biomass that were used to condition each individual OM model.

	OM1	OM2	OM3	OM4
Female M	0.184	0.213	0.215	0.15
Male M	0.164	0.178	0.203	0.147
SigmaR	0.50	0.50	0.54	0.54
Conditioning SB	Long AAF	Short AAF	Long CW	Short CW

The models were conditioned to four general sources of information:

- Predicted spawning biomass estimated from the corresponding stock assessment (Table 9).

- Fishery Independent Setline Survey (FISS) indices of abundance for each Biological Region.

- FISS estimates of proportions-at-age for each Biological Region. This component was downweighted compared to other components.

- Proportion of all-sizes weight-per-unit-effort (WPUE) in each Biological Region from the space-time model analysis of FISS observations. This is also called stock distribution and was given the highest weight as this is an important component for the OM to mimic.

Table 10: Descriptions of the parameters estimated when conditioning the OM. Separate sets of parameters were estimated for movement in poor and good PDO regimes.

Parameters	# parameters	Description
$\ln(R_0)$	1	Natural log of unfished equilibrium recruitment. Determines the scale of the population trajectory.
$p_{y,r}^R$	6	Proportion of R_0 distributed to each Biological Region. Only three of the four parameters need to be estimated to sum to 1. An adjustment is estimated for high PDO (i.e. good environmental regime).
p^I	1	A multiplier on initial fishing mortality, which increased or decreased the initial fishing mortality input to initialize the population.
$\Psi_{3\to2}$	5 + 5	Probability of movement-at-age from Region 3 to Region 2, modelled using a double-exponential function (equation 3). The left and right λs, left maximum probability, right maximum probability, and right asymptote were estimated. The probability at any age could not exceed 0.7.
$\Psi_{4\to3}$	5 + 5	Probability of movement-at-age from Region 4 to Region 3, modelled using a double-exponential function (equation 3). The left and right λs, left maximum probability, right maximum probability, and right asymptote were estimated. The probability at any age could not exceed 0.7.

The lognormal likelihood (assuming that the observed value was the median) was used to fit to the predicted stock assessment spawning biomass and the survey indices.

$$-\ln(L) = \sum \left(\frac{\ln\left(O_y / E_y\right)}{\sigma_y} \right)^2 \tag{51}$$

where O_y is the predicted spawning biomass from the stock assessment, E_y is the predicted spawning biomass from the OM, and σ_y is the standard deviation of the stock assessment spawning biomass on a natural log scale calculated as $\sigma_y = \sqrt{ln(1 + cv^2)}$.

A robustified multivariate normal (Fournier et al 1990, Starr et al 1999) was used to fit to the survey proportions-at-age and the regional stock distribution estimates.

$$-\ln(L) = -\sum \ln \left[\exp\left(\frac{-(O_y - E_y)^2}{2O_y'/N'} + 0.01 \right) \right] \tag{52}$$

where $O_y' = \left(1 - O_y\right)O_y + 0.1/n$ and N' is the effective sample size as entered in the stock assessment (before data weighting). Estimates of uncertainty were available for the proportion of survey biomass in each Biological Region, thus the denominator was the standard deviation instead of O'_y/N'.

The parameters in Table 10 were fit to the four data sources individually to determine similarities and differences in the estimates of parameters and derived quantities that each data source implied. This was done for different parameterizations of movement to understand how changes to the structure affected the fit to the different data sets. Those results (not shown here) identified that fitting to the modelled survey distribution of biomass in each Biological Region was important because fitting to no other single data source resulted in a close prediction of the distribution. Stock distribution is an important component of many management procedures to be tested, thus must be represented accurately by the conditioned OM. Secondly, fitting to index data resulted in predicted spawning biomass trajectories that were generally in the envelope of predicted spawning biomass from the stock assessment models. Index data are an important data source as they reflect trends in abundance by Biological Region. Fitting to proportion-at-age did not greatly improve the overall

general trends in recent estimates of proportion-at-age in each region but did result in low predicted spawning biomass. The conditioning was heavily weighted to the stock distribution and spawning biomass components. The goal was to have models adequately predicting stock distribution and spawning biomass in recent years, with some variability.

3.4.2.2 *Uncertainty in the conditioned operating model*
Uncertainty in population trajectories was captured by adding variability to the parameters of the operating model as specified in Table 7. Variances and covariances of parameters estimated in the conditioning process were estimated from the inverse of the Hessian. However, due to multicollinearity and difficulty in finding optimal solutions when all parameters were estimated[2], some parameters were fixed to estimate the Hessian and then supplied a small variance. The correlation matrix estimated from the corresponding 'long' stock assessment model with steepness estimated (the long stock assessment models were run with a broad prior on steepness only to determine variability in steepness through estimation of the Hessian), was used as uncertainty in steepness, natural mortality (female and male), and recruitment deviation parameters. This was combined with the correlation matrix for the R_0, initial multiplier on fishing mortality, movement, and recruitment distribution parameters as estimated from the conditioning process. The covariance matrices from the conditioning and assessment models were combined without accounting for correlation in parameters between the two sources (assessment or OM), but correlations between parameters were accounted for within each source.

The combined covariance matrix was used to sample from a truncated multivariate normal distribution to provide replicate parameter sets for each OM model, providing multiple trajectories from 1958 through 2022 for each model. Bounds were enforced on some parameters, hence the truncated multivariate normal distribution. For example, steepness was bounded between 0.6 and 0.98, probability parameters associated with movement parameterizations were bounded between 0 and 1, and the natural log of recruitment deviations were bounded between -4 and 4. In a few uncommon cases, the standard deviation of a parameter had to be reduced because it was often exceeding a bound (e.g. probability parameters near zero). Parameter sets that resulted in unrealistically low population sizes or extremely poor fits to stock distribution or spawning biomass were rejected determined from the likelihood for the fit to stock distribution and the total likelihood. The likelihood thresholds were an *ad hoc* three times the likelihood achieved from conditioning, based on visual fits to the data and investigation of outputs at various likelihood values. This is second step is required because some correlations between parameters are not accounted for resulting in unrealistic combinations.

3.4.2.3 *Conditioned operating model*
The four OM models showed important structural differences in terms of movement rates-at-age, recruitment distribution, and historical spawning biomass trends. The four individual models in the OM show significantly different historical spawning biomass trajectories before the early 2000s and subtle differences in recent years (Figure 31). Relative spawning biomass differs between the four individual models because of different assumptions about productivity (Figure 31). These differences stem from the different assessment models in the ensemble assessment and are attributable to the very different assumptions about how the stock was distributed and connected via movement in relation to historical fishing mortality. It is important to capture these differences through movement and distribution in the OM.

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[2] The function 'optim' was used in R with abrupt penalties enforced when spawning biomass was predicted below a small inconceivable value or when parameters were out of pre-specified bounds.
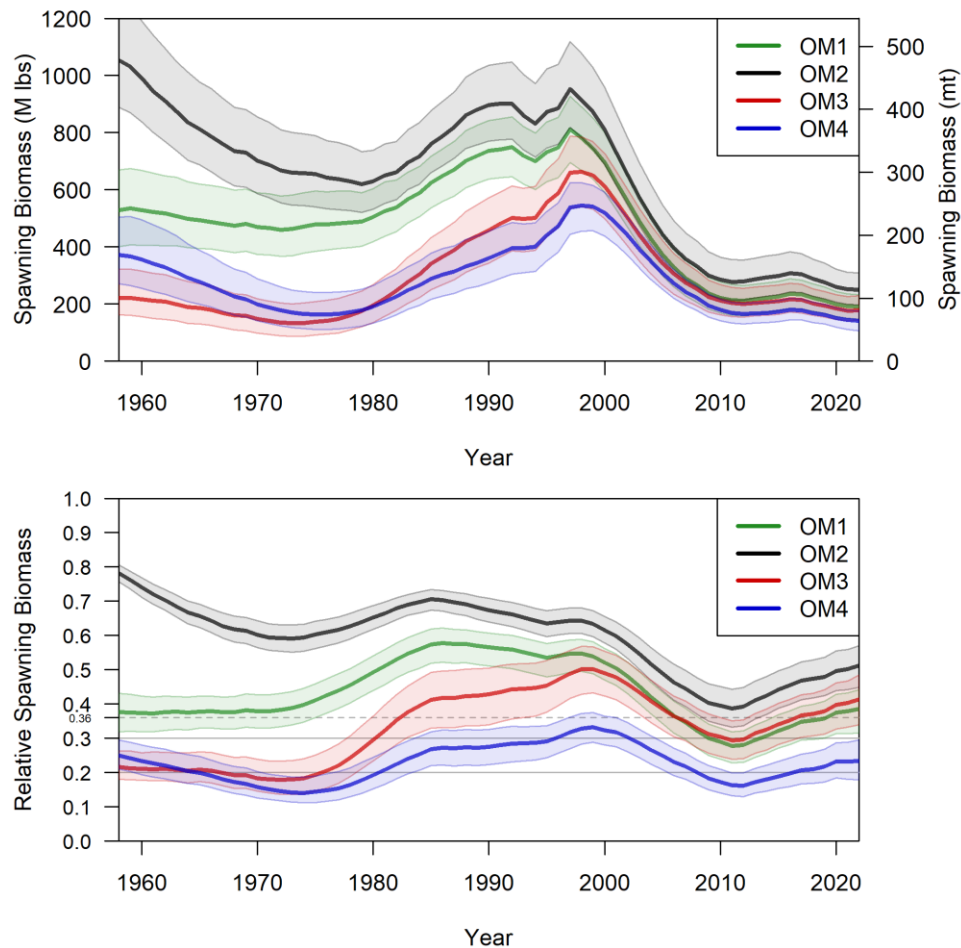
Figure 31. Estimated spawning biomass trajectories (top) and relative spawning biomass trajectories (bottom) from 1958 to 2022 for each individual model in the OM.

The OM with the four individual models combined show an uncertainty that is slightly broader in recent decades than the 2022 ensemble stock assessment uncertainty (Figure 32). Median spawning biomass was nearly the same for the OM and the ensemble stock assessment. Uncertainty in projections is large due to variability in weight-at-age and recruitment.

Stock distribution was fit well by each OM model (Figure 33) and showed very similar patterns of lack of fit for each individual model in some years. Specifically, the earliest years in Biological Region 4 were overfit by the OM, and recent years overfit in Biological Region 3 corresponding with a slight underfitting in region 2. Each individual model showed small differences in fits and trends to recent years. The all-sizes stock distribution for the OM, integrated over the individual models, is shown in Figure 34.

Distributions used for sex-specific natural mortality (M) varied between the OM individual models (Figure 35) spanning the range of natural mortality values used in the 2022 stock assessment. The distributions of steepness were similar for the individual models (Figure 36).
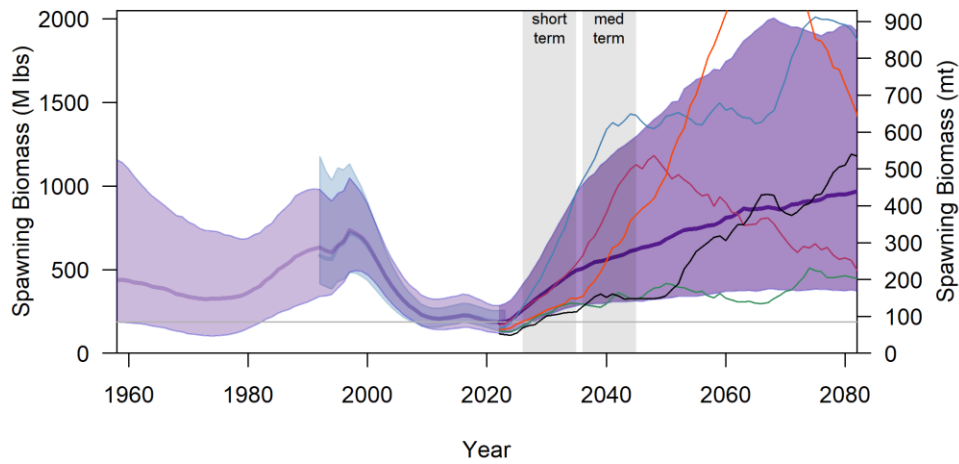
Figure 32. Median, 5th, and 95th quantiles for the OM (purple) and the ensemble assessment (blue). Projections starting in 2023 with no fishing mortality are shown in darker colors. Trajectories from individual replicates are shown as thin lines of various colors. Short-term and medium-term grey bands show time-periods defined by the IPHC for evaluation.
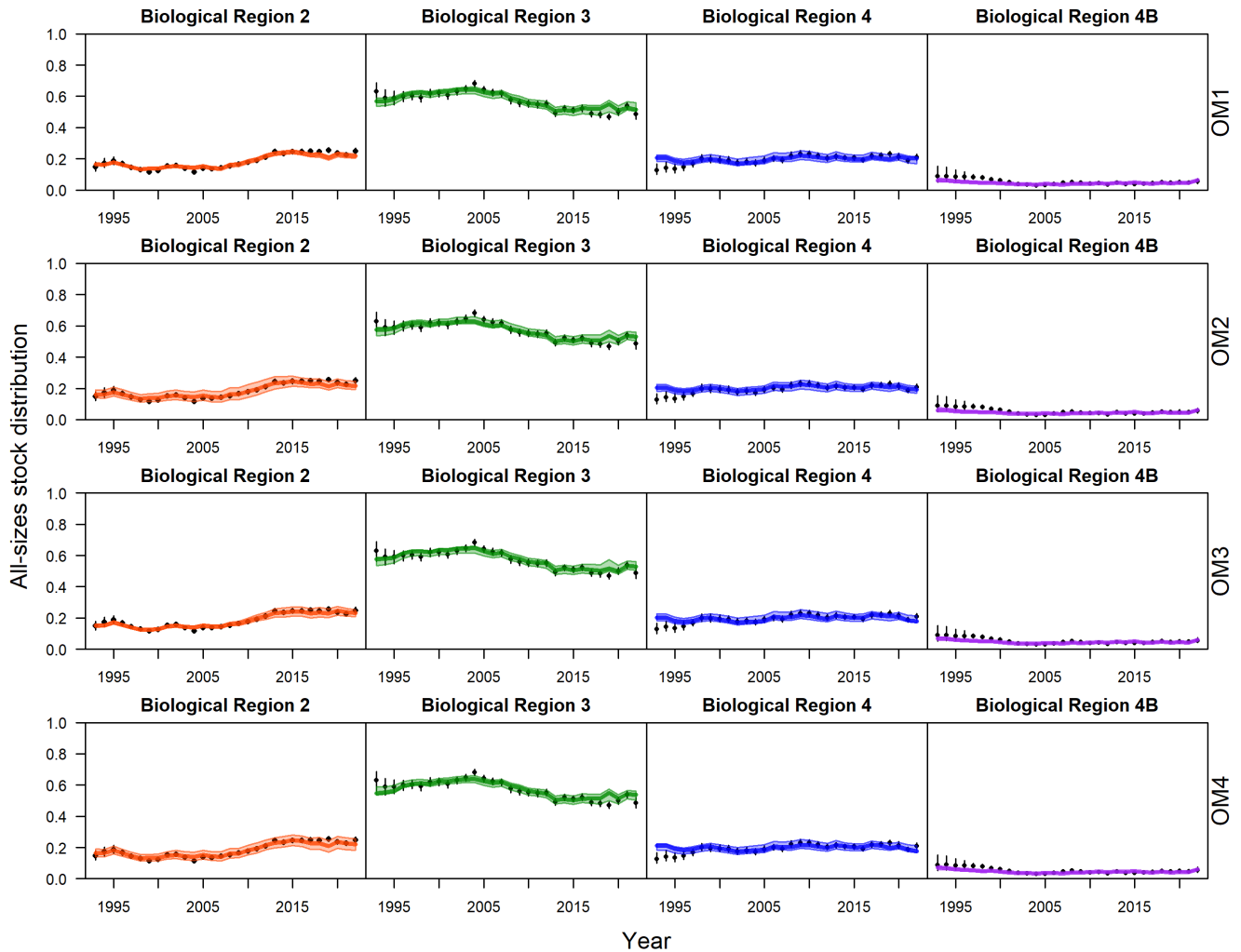

Figure 33: Stock distribution determined from FISS observations (points and vertical bars for the median and 90% confidence interval) and from each OM model with variability (shaded areas) showing the 5th and 95th percentiles.
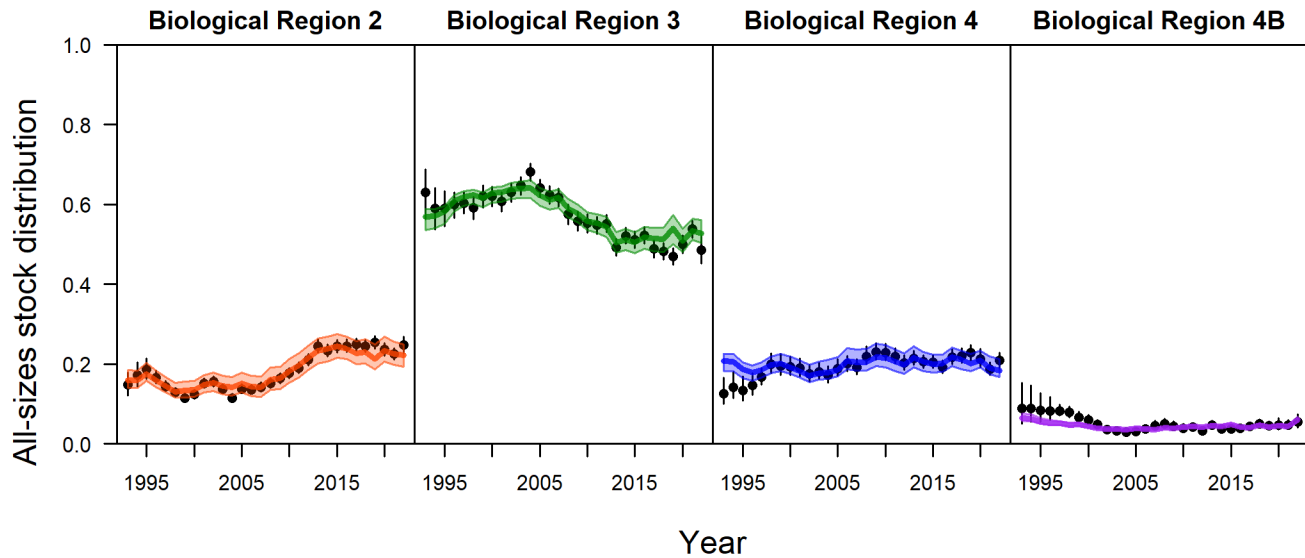
Figure 34. Stock distribution determined from FISS observations (points and vertical bars for the median and 90% confidence interval) and integrated over all individual OM models with variability (shaded areas) showing the 5th and 95th percentiles.

The distribution of age-0 recruits showed a high proportion going to Biological Region 4 in both low and high PDO regimes. Sadorus et al. (2020) found that recruits were more likely to end up in the Bering Sea in "warm years" for most spawning areas in the Gulf of Alaska. Furthermore, "cold years" were likely to have less dispersal to the west in the Bering Sea and "warm years" were more likely to have more dispersal to the northwest from spawning in the Western Gulf of Alaska. OM1 was the only Individual OM model that did not show a higher proportion of recruits going to Biological Region 4 in high PDO years, but was similar between PDO regimes (Figure 37). OM1 did show more age-0 recruits in Biological Region 3 in high PDO years with a reduced proportion of recruits in Biological Region 2.

Movement rates between Biological Regions 3 and 2, and Biological Regions 4 and 3 differed slightly between the four individual OM models (Figure 38). The lifetime probability of moving from one area to another is calculated as one minus the product of the age-specific probabilities of not moving from one region to the other region. There was an over 80% chance that a fish would move from Biological Region 4 to Biological Region 3 over its lifetime in either PDO regime. There was a high chance that a fish would move from Biological Region 3 to Biological Region 2 over its lifetime in a low PDO regime, but a small chance for three of the four individual OM models in a high PDO regime. Movement rates were generally highest between ages 3 and 6 years, with OM2 showing movement rates-at-age as high as 0.7. The models sometimes had difficulty determining if one or two ages had high movement rates or if movement was spread across a wider range of ages at a lower rate.
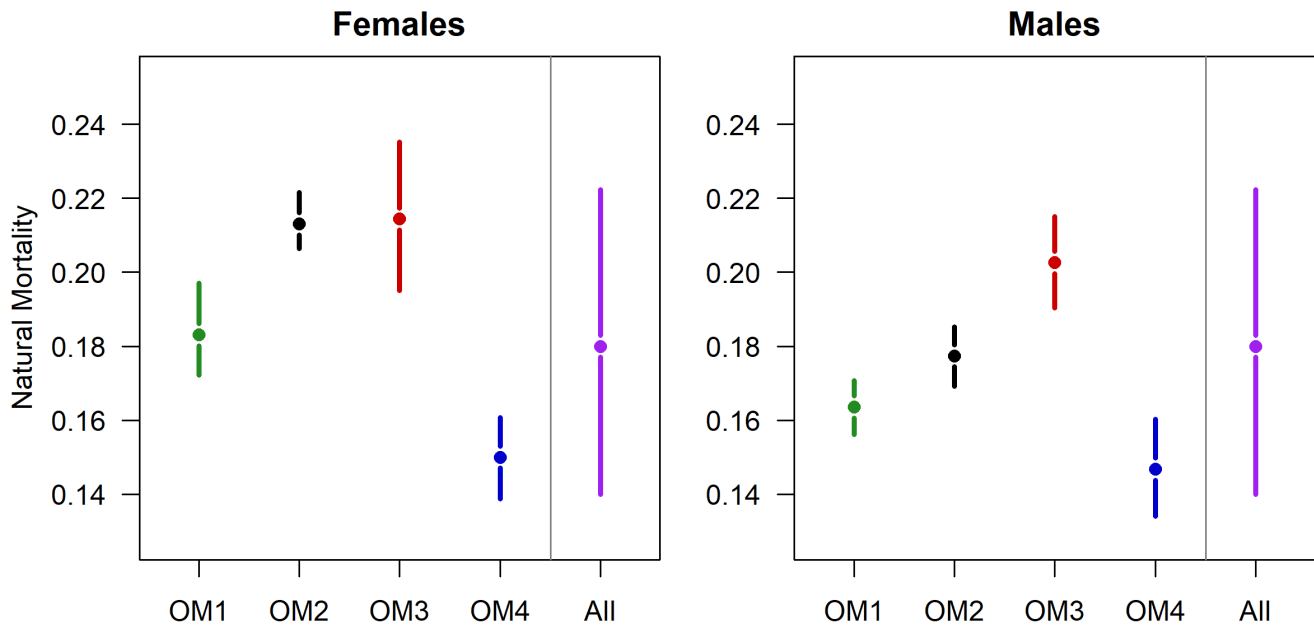
Figure 35. Natural mortality (*M*) distributions from 500 replicates used to create multiple trajectories of the OM individual models and the integrated OM (All) for females and males.
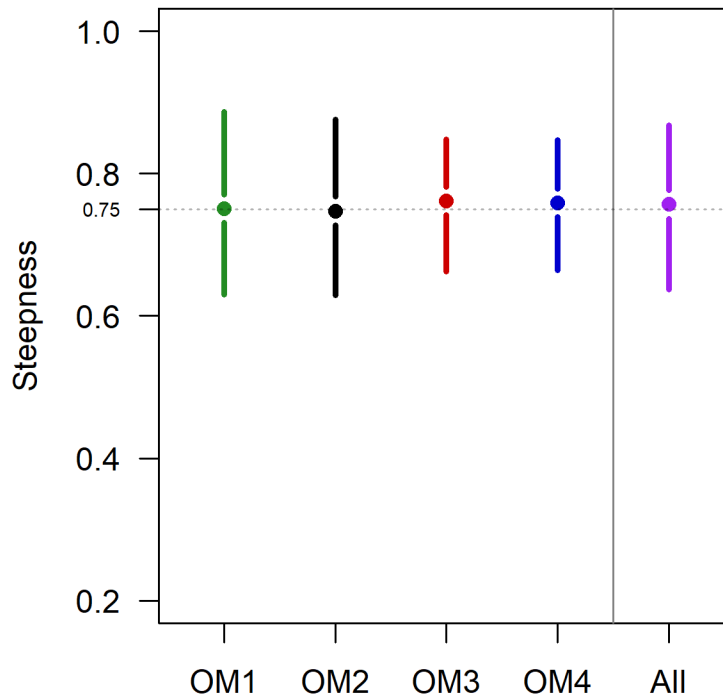

Figure 36. Steepness (*h*) distributions from 500 replicates used to create multiple trajectories of the OM individual models and the integrated OM (All).
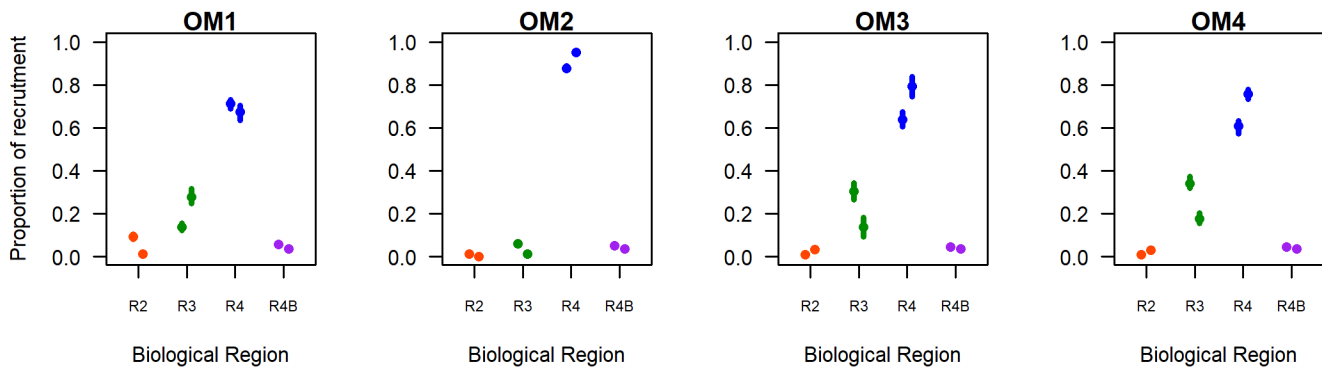
Figure 37. Proportion of recruits in each Biological Region (colors) for low and high PDO regimes (adjacent same color) for individual OM models.
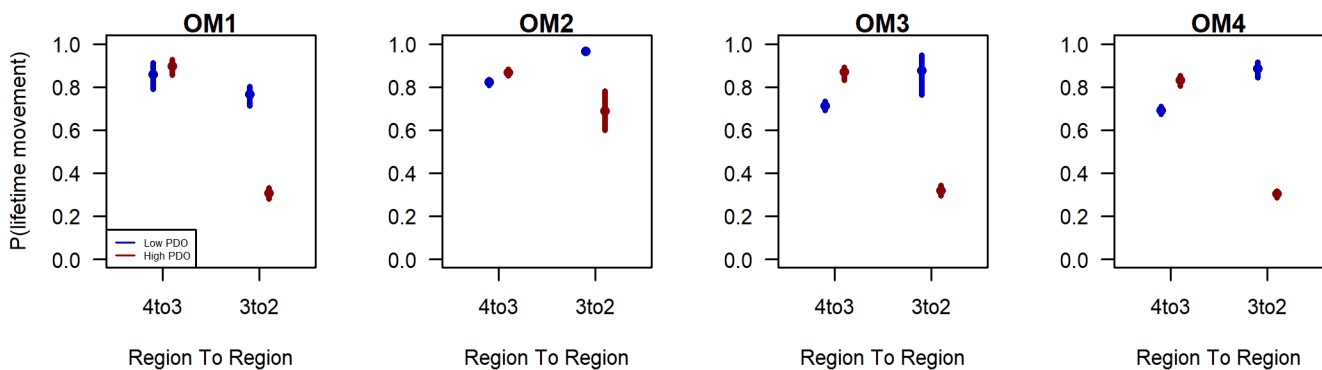

Figure 38. Probability of movement-at-age from Biological Region 3 to region 2 (top) and region 4 to region 3 (bottom) in low PDO (left) and high PDO (right) regimes for the two OM models.

Overall, the conditioned multi-region OM, composed of two models, represents the general trends of the Pacific halibut population, characterizes uncertainty and variability, and is a useful model to simulate the population forward in time and test management strategies. There are many changes to the model and conditioning process that could be made to potentially improve these fits. For example, movement may be sex-specific, but tagging data are lacking this information.

Projections with the OM incorporating parameter variability (Table 7) and projection variability (Table 8) produced a wide range of trajectories. Figure 31 shows the variability in historical trajectories for each individual OM model, and Figure 32 shows the range of integrated trajectories with five example individual trajectories with variable weight-at-age and environmental regime switching, while assuming no fishing mortality. An individual trajectory may cover a wide range of spawning biomass values in this 60-year period.

3.4.3 Simulation process

A framework was developed to conduct simulations. With the conditioned OM, individual trajectories are run from an R script. The OM internally calls an R script annually in the projection to invoke the MP and any other externally simulated processes. At the end of that projection the OM quits and the original R script compresses and saves the output to a specified folder. This loops through all of the OM trajectories (simulations) to produce multiple folders of output. Post-processing of the output is done to create the desired performance metrics and reduce the output into a single Rdat file, which is then summarized into tables and figures for evaluation.

3.4.4 Performance metrics and evaluation of results

Performance metrics were defined for the primary objectives. However, to assist in the evaluation of tradeoffs between different MPs, additional performance metrics were defined with input from the Management Strategy Advisory Board (MSAB). All performance metrics are calculated as short-term (4-13 years), medium-term (14-23 years), and long-term (10-year period in equilibrium) metrics. For a complete list of the performance metrics available please visit the MSE Explorer page.

The MSE Explorer website is an interactive tool that is useful to examine and filter results. MSE Explorers of results from various meetings are archived at http://iphcapps.westus2.cloudapp.azure.com/. The most recent version of MSE Explorer is at the following URL.

http://iphcapps.westus2.cloudapp.azure.com/MSE-Explorer/

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5 APPENDICES

Appendix I: Parameters and notation

Appendix II: Fishing Mortality using Exploitation Rate: Two Approaches

Appendix III: Primary objectives defined by the Commission for the MSE

Appendix I
Parameters and Notation

Table I.1: Dimension and partition notation in the operating models (used as subscripts).

Parameter	Description
y	Time-step, typically annual and may be thought of as a year.
a	Age. A capital A indicates the maximum age.
s	Sex, which includes female, male, and unsexed, in that order, labeled 1, 2, and 3.
r	Region with movement occurring between regions.
r_l	Area within region. Movement is not modelled between areas.
im	Immature state of the maturity partition.
ma	Mature state of the maturity partition.
sp	Spawning state calculated from the maturity partition. Note that this is not a specific partition in the state object.
sr	Selected and retained in reference to a particular fishery
f	Fishery sector.
I	Initial, meaning the starting time-step.

Table I.2: Parameters in the operating models.

Parameter	Description
Population dynamics parameters	
$N_{a,s|t,r}$	Numbers for age, sex, time, and region
B_0	Unfished equilibrium biomass
R_0	Unfished equilibrium recruitment
$B_{a,s|t,r}$	Biomass at the beginning of time t (and possibly other partitions as noted)
$B_{a,s|t,r}^M$	Mature biomass at the beginning of time t
$B_{a,s|t,r}^S$	Spawning biomass at the beginning of time t
$B_{|t,r,f}^{sr}$	Biomass selected and retained by fishery f at time t
$M_{a,s|t,r}$	Natural mortality
$W_{a,s|t,r}$	Mean weight-at-age in year t (and possibly other partitions)
$\Omega_{a,s|t,r}$	Proportion of mature individuals at age.
$\Phi_{a,s|t,r}$	Proportion of spawning individuals at age
$\Psi_{j \to k}$	Movement rate from area j to area k. partitioned into age, sex and time.
$p_{t,r}^R$	Proportion of fish recruited to region r at time t.
p_s^R	Proportion of females at birth.
p_f	Proportion of mortality that occurs before exploitation from fishery f occurs.

Table I.2 continued.

Parameter	Description
Fishing mortality related parameters	
$C_{a,s|t,r,f}$	Catch (in weight) for age, sex, time, region, and fishery. Catch summed over age and sex ($C_{|t,r,f}$) is typically an input to the model.

$C_{a,s|t,r,f}^{N}$ Catch (in numbers) for age, sex, time, region, and fishery.

$U_{y,r,f}$ Exploitation rate for fishery f

$S_{a,f}$ Selectivity-at-age for fishery f

$T_{a,f}$ Proportion retained-at-age for fishery f

Index parameters

I_t^{sur} Survey index for time *t* in region *r.* May be 'all-sizes' (*surAll*) or O32 (*surO32*)

$q_{t,r}^{sur}$ Survey catchability for year *t* and region *r*

ε_t^{sur} Error at time *t* for the survey series in region *r*

$I_{t,r}^{comm}$ CPUE index for the directed commercial fishery in time *t* and region *r.*

$q_{t,r}^{comm}$ CPUE catchability for year *t* and region *r*

$\varepsilon_{t,r}^{comm}$ Error in year *t* for the CPUE series in region *r*

Appendix II
Fishing Mortality using Exploitation Rate: Two Approaches

This appendix presents two methods to determine catch and exploitation rates when modelling the fisheries with an exploitation rate (finite or Pope's approximation) instead of the instantaneous formulation (i.e. Baranov equation). The benefit of using an exploitation rate is that the code does not have to iterate to find the fishing mortality rate (i.e., there is not closed-form solution for the Baranov formulation). This will speed up the simulation time.

These equations have been simplified to show the concept. For example, retention and discard mortality are not considered, and sex and region subscripts have been omitted. The subscripts remaining are a for age, t for time-step, and f for fleet/fishery. Superscripts are used to indicate specific about the quantity, such as n for numbers and sr for selected-retained (i.e., exploitable by a particular fleet), as well as the timing within the time-step (e.g., 0.25 would be one-quarter of the natural mortality in that time-step occurred).

Fisheries are independent and do not affect each other

To make things simpler, in a sense, we may make the assumption that the fisheries are independent of each other or they occur at exactly the same time. That means that the sequential nature of the fisheries does not have to be tracked, making the equations and accounting simpler. However, an additional complication is introduced in making sure that the total exploitation rate (sum over all fisheries) does not exceed a defined maximum (or a value of one).

Fishing mortality is parameterized with an exploitation rate and is assumed to occur at a specific point in time after a proportion of the mortality ($p_{|f}$) has occurred. The proportion may be equal for all fleets, and if not then it is assumed that the removals from a fleet operating before other fleets does not affect the biomass available to subsequent fleets (may be OK with small exploitation rates).

Catch at age and sex in numbers (C^n) or weight (C) for a sector in an area can be determined from the exploitation rate (U), selectivity (S), and mean weight-at-age (W). Note that retention is not listed to simplify the examples shown here.

$$
\begin{aligned}
C^n_{a|t,f} &= U_{|t,f} N_{a|t} S_{a|t,f} e^{-p_f M_{a|t}} \\
C_{a|t,f} &= U_{|t,f} N_{a|t} S_{a|t,f} W_{a|t,f} e^{-p_f M_{a|t}}
\end{aligned}
$$

and the total predicted catch for a sector in a region is

$$
\begin{aligned}
C^n_{|t,f} &= \sum_{a=0}^{A} C^n_{a|t,f} \\
C_{|t,f} &= \sum_{a=0}^{A} C_{a|t,f} = U_{|t,f} B^{sr,p}_{|t,f}
\end{aligned}
$$

Natural and fishing mortality can be accounted for simultaneously, and the numbers-at-age in the next time-step, after all mortality, can be simply determined with a single equation. Let's assume there are two fleets with the mortality from fleet 1 occurring after three fifths of the natural mortality ($p_{|1} = 0.6$) and the mortality from fleet 2 occurring after one-quarter of the natural mortality ($p_{|2} = 0.25$). The catch (in numbers) for each fleet is

$$
\begin{aligned}
C^n_{a|t,f=1} &= N_{a|t} U_{|t,f=1} S_{a|t,f=1} e^{-0.6 M_a} \\
C^n_{a|t,f=2} &= N_{a|t} U_{|t,f=2} S_{a|t,f=2} e^{-0.25 M_a}
\end{aligned}
$$

The numbers-at-age in the next year, accounting for fishing mortality by removing the catch at the appropriate time, is

$$N_{a|t+1} = \left[[N_{t,a}e^{-0.25M_a} - C^N_{a|f=2}]e^{-(0.6-0.25)M_a} - C^N_{a|f=1}\right]e^{-(1-0.6)M_a}$$

Converting the catch (C^n) to exploitation rates using equation for $C^n_{a|t,f=1}$ and simplifying produces the equation for N in the next time-step.

$$
\begin{aligned}
N_{a|t+1} &= \left[[N_{t,a}e^{-0.25M_a} - N_{a|t}U_{|t,f=2}S_{a|t,f=2}e^{-0.25M_a}]e^{-(0.6-0.25)M_a} - \right. \\
&\qquad \left. N_{a|t}U_{|t,f=1}S_{a|t,f=1}e^{-0.6M_a}\right]e^{-(1-0.6)M_a} \\
&= \left[N_{t,a}e^{-0.25M_a}e^{-0.35M_a}(1 - U_{|t,f=2}S_{a|t,f=2}) - N_{a|t}U_{|t,f=1}S_{a|t,f=1}e^{-0.6M_a}\right]e^{-0.4M_a} \\
&= \left[N_{t,a}e^{-0.6M_a}(1 - U_{|t,f=2}S_{a|t,f=2}) - N_{a|t}U_{|t,f=1}S_{a|t,f=1}e^{-0.6M_a}\right]e^{-0.4M_a} \\
&= \left[N_{t,a}e^{-0.6M_a}(1 - U_{|t,f=2}S_{a|t,f=2} - U_{|t,f=1}S_{a|t,f=1})\right]e^{-0.4M_a} \\
&= N_{t,a}e^{-M_a}\left(1 - \sum_f U_{|t,f}S_{a|t,f}\right)
\end{aligned}
$$

This can be generalized to any set of $p_{|f}$ as long as the proportions are sorted from smallest to largest in the derivation. The sequential nature of the fleets does not need to be accounted for in the calculations.

However, a potential problem is that the sum of the exploitation rates may exceed a value of one (or some defined maximum), which is theoretically impossible. Therefore, a maximum exploitation rate (U_{max}) must be specified, which is realistically less than one. To determine if the overall exploitation rate is greater than U_{max}, the partition-specific exploitation rates (e.g., age, sex, region, and fleet) for a time-step are summed across fleets within a region, and the maximum rate within a region over the partions are determined. This is called U_y^{maxObs}.

$$U_{|t}^{maxObs} = max_a\left(\sum_f S_{a|t,f}U_{|t,f}\right)$$

If $U_y^{maxObs} > U_{max}$, then

$$U_{|t,f} = \frac{U_{max}}{U_{|t}^{maxObs}}\frac{C_{|t,f}}{B_{|t,f}^{sr,p}}$$

which is simply an adjustment to the original exploitation rate ($U_{|t,f}$). When this adjustment occurs, the predicted catch will be different than the input catch, and a penalty should be applied since catches are considered observed inputs (not data with error).

Catch is an input and biomass is calculated as part of the modelling process, so the exploitation rate is calculated as the ratio between catch and exploitable biomass for a particular fleet.

$$U_{|t,f} = \frac{C_{|t,f}}{B_{|t,f}^{sr,p}}$$

where $C_{|t,r,f}$ is the catch in time-step t and region r for sector f, and $B_{|t,r,f}^{sr}$ is the selected-and-retained (exploitable) biomass for that fishery.

The exploitable biomass is calculated from the numbers-at-age (N), selectivity (S), and mean weight-at-age (W).

$$B_{|t,f}^{sr,p} = \sum_{a=0}^{A} N_{a|t}S_{a|t,f}W_{a|t,f}e^{-p_{|f}M_{a|t}}$$

Fisheries are sequential and earlier fisheries effect later ones

The more appropriate way to model the fisheries, but more complex in terms of accounting, is to account for the decline in the population from fisheries occuring before later fisheries. For example, as above, let's assume there are two fleets with the mortality from fleet 1 occurring after three fifths of the natural mortality ($p_{|1} = 0.6$) and the mortality from fleet 2 occurring after one-quarter of the natural mortality ($p_{|2} = 0.25$). The "pulse" fishing activity of fleet 2 causes a reduction in the population by the time fleet 1 operates its fishery, and the catch (in numbers) for each fleet would be calculated as follows.

$$
\begin{aligned}
C_{a|t,f=2}^n &= N_{a|t}e^{-p_2 M_{a|t}}U_{|t,2}S_{a|t,2} \\
C_{a|t,f=1}^n &= \left(N_{a|t}e^{-p_2 M_{a|t}} - C_{a|t,f=2}^n\right)U_{|t,1}S_{a|t,1}e^{-(p_1-p_2)M_{a|t}} \\
&= \left(N_{a|t}e^{-p_2 M_{a|t}} - U_{|t,2}S_{a|t,2}e^{-p_2 M_{a|t}}N_{a|t}\right)U_{|t,1}S_{a|t,1}e^{-(p_1-p_2)M_{a|t}} \\
&= N_{a|t}e^{-p_2 M_{a|t}}\left(1 - U_{|t,2}S_{a|t,2}\right)U_{|t,1}S_{a|t,1}e^{-(p_1-p_2)M_{a|t}} \\
&= N_{a|t}e^{-p_1 M_{a|t}}\left(1 - U_{|t,2}S_{a|t,2}\right)U_{|t,1}S_{a|t,1}
\end{aligned}
$$

Generally,

$$
C_{a|t,f}^n = U_{|t,f}S_{a|t,f}e^{-p_f M_{a|t}}N_{a|t}\prod_{f' \in p_{j\neq f}<p_f}\left(1 - U_j S_{a|t,f'}\right)
$$

where $(1 - U_j S_{a|t,f'})$ is the probability of surviving a fishery that occurs before the fishery for fleet f. This requires some additional logic to determine which fisheries have occurred before the fishery of interest to properly account for that preceeding mortality.

The numbers-at-age in the next time-step can be derived in a similar manner as above, except using the newly defined catch equations.

$$
N_{a|t+1} = \left[\left[N_{t,a}e^{-0.25M_a} - C_{a|f=2}^N\right]e^{-(0.6-0.25)M_a} - C_{a|f=1}^N\right]e^{-(1-0.6)M_a}
$$

Converting the catch (C^N) to exploitation rates using the equation for $C_{a|t,f}^n$ and simplifying produces the equation for N in the next time-step.

$$
\begin{aligned}
N_{a|t+1} &= \Big[\big[N_{a|t}e^{-0.25M_a} - N_{a|t}U_{|t,f=2}S_{a|t,f=2}e^{-0.25M_a}\big]e^{-(0.6-0.25)M_a} - \\
&\quad N_{a|t}U_{|t,f=1}S_{a|t,f=1}e^{-0.6M_a}(1 - U_{|t,f=2}S_{a|t,f=2})\Big]e^{-(1-0.6)M_a} \\
&= \Big[N_{a|t}e^{-0.6M_a}(1 - U_{|t,f=2}S_{a|t,f=2}) - N_{a|t}U_{|t,f=1}S_{a|t,f=1}e^{-0.6M_a}(1 - U_{|t,f=2}S_{a|t,f=2})\Big]e^{-0.4M_a} \\
&= \Big[N_{a|t}e^{-0.6M_a}(1 - U_{|t,f=2}S_{a|t,f=2})(1 - U_{|t,f=1}S_{a|t,f=1})\Big]e^{-0.4M_a} \\
&= N_{a|t}e^{-M_a}\prod_f\left(1 - U_{|t,f}S_{a|t,f}\right)
\end{aligned}
$$

This is simply the numbers-at-age in the current time-step times the survival from natural causes times the survival from each fishery. With this formulation, adjusting for a maximum exploitation rate is not necessary, other than ensuring that each fleet-specific exploitation rate does not exceed a value of one (or a defined maximum).

Catch is an input and biomass is calculated as part of the modelling process, so the exploitation rate is calculated as the ratio between catch and exploitable biomass for a particular fleet.

The exploitable biomass is calculated from the numbers-at-age (N), selectivity (S), and mean weight-at-age (W), and accounts for the decrease in abundance due to fisheries that occurred previously.

$$B^{sr,p}_{|t,f=2} = \sum_{a=0}^{A} N_{a|t}S_{a|t,2}W_{a|t,2}e^{-p_{|2}M_{a|t}}$$

$$B^{sr,p}_{|t,f=1} = \sum_{a=0}^{A} \left(N_{a|t}e^{-p_{|2}M_{a|t}} - C^{n}_{a|t,2}\right)S_{a|t,1}W_{a|t,1}e^{-(p_{|1}-p_{|2})M_{a|t}}$$

$$= \sum_{a=0}^{A} \left(N_{a|t}e^{-p_{|2}M_{a|t}} - U_{|t,2}S_{a|t,2}e^{-p_{2}M_{a|t}}N_{a|t}\right)S_{a|t,1}W_{a|t,1}e^{-(p_{|1}-p_{|2})M_{a|t}}$$

$$= \sum_{a=0}^{A} N_{a|t}e^{-p_{|2}M_{a|t}}\left(1 - U_{|t,2}S_{a|t,2}\right)S_{a|t,1}W_{a|t,1}e^{-(p_{|1}-p_{|2})M_{a|t}}$$

$$= \sum_{a=0}^{A} N_{a|t}e^{-p_{|1}M_{a|t}}\left(1 - U_{|t,2}S_{a|t,2}\right)S_{a|t,1}W_{a|t,1}$$

which is the same result if using the equation $C = U \times B$.

Comparison

It can be shown that these two assumptions produce the exact same results when only one fishery is considered. When two or more fisheries occur at exactly the same time, the catch is exactly the same (i.e., one fishery does not occur before another, thus they operate on the same biomass), but the equation for N_{t+1} is slightly different between the two formulations. Say that two fisheries operate 3/5ths of the way through the time-step, each with an exploitation rate of 0.5. If they operated independently and each took half of the exploitable biomass, then all of the exploitable biomass would be removed since the sum of the two exploitation rates is 1. The real issue comes in when the sum of the exploitation rates is greater than 1, which is theoretically impossible.

Using the above two fisheries occurring at exactly the same time, let's assume that the exploitation rates were 0.3 and 0.4, which is still quite high for a marine commercial fishery. That is a combined exploitation rate 0.7 (assuming selectivity equals 1) and the equations for abundance in the next year are

$$\text{Independent fisheries} = N_{a|t}e^{-M_a}[1 - (0.3 + 0.4)] = N_{a|t}e^{-M_a}(0.3)$$
$$\text{Sequential fisheries} = N_{a|t}e^{-M_a}(1 - 0.3)(1 - 0.4) = N_{a|t}e^{-M_a}(0.42)$$

Therefore, the number-at-age is 1.4 times greater for the sequential fishery compared to the independent fisheries. This occurs because of the product of the two exploitation rates is added back in, when expanded.

$$\text{Independent fisheries} = [1 - (U_1 + U_2)] = (1 - U_1 - U_2)$$
$$\text{Sequential fisheries} = (1 - U_1)(1 - U_2) = (1 - U_1 - U_2 + U_1U_2)$$

This is especially useful when the exploitation rate is high because it never allows the exploitation rate to exceed one. For example, when U=1 (the theoretcial maximum) the independent fisheries equation results in a multiplier of -1, while the sequential fisheries equation results in a multiplier of 0. When exploitation rates are 0.2 for two fisheries, the difference between the two methods is small (i.e., $0.2 \times 0.2 = 0.04$ and 1.07 times greater for the sequential fisheries). Additionally, exploitation rates in the sequential method are more interpretable as exploitation rates and do not need adjustments to make them remain below the theoretical maximum of one. Figure Figure 39 shows that are small exploitation rates, the difference in survival between the two methods is small.
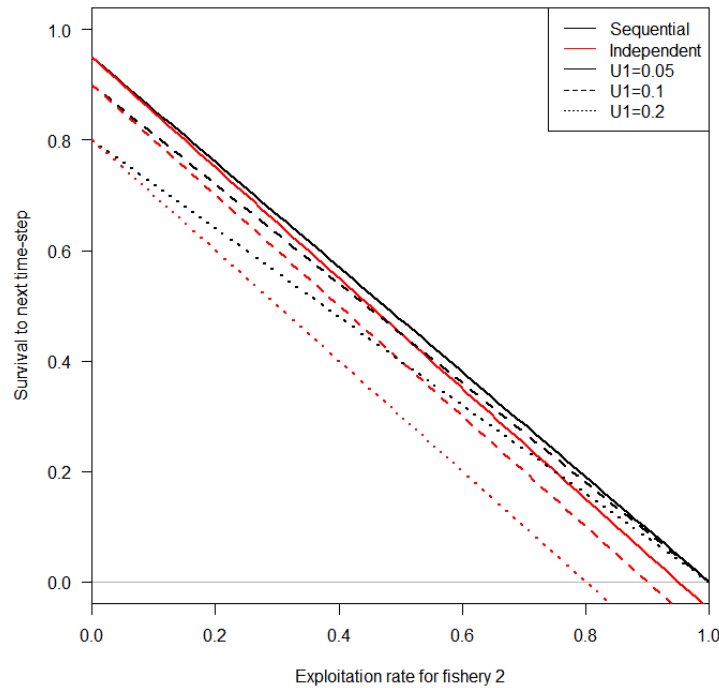
Figure 39: A comparison of survival to the next-time step for the sequential (black) and independent (red) methods assuming exploitation rates (**U**) of 0.05, 0.1, and 0.2 for fishery 1, and a range of exploitation rates for fishery 2.

It is unlikely that two fisheries operate independently when exploitation rates are high and it may be more prudent to treat them in a sequential nature, calculating the exploitation rates for each from the sequential exploitable biomass (or splitting them up into many catch events and switching back and forth between the two, which is overly complicated). We propose to use the equations under the sequential fisheries, and when two or more fisheries operate at the exact same time, the fishery operates in a sequence in order of the size of their catch for that time-step (smallest to largest).

A more complex example with three fisheries and discard mortality

It is worth working through the concept of sequential fisheries when three fisheries occur and each has discard mortality. Let's assume there are three fleets with the mortality from fleet 1 occurring after one-fifth of the time-step ($p_{|1} = 0.2$), the mortality from fleet 2 occurring after two-fifths of the time-step ($p_{|2} = 0.4$), and the mortality from fleet 3 occurring after four-fifths of the time-step ($p_{|2} = 0.8$). The total mortality (in numbers) includes catch and discard mortality for each fleet and would be calculated as follows (with the current time-step subscript (t) removed for simplicity).

$$
\begin{aligned}
TM^n_{a|f=1} &= C^n_{a|1} + D^n_{a|1} \\
&= N_a e^{-p_1 M_a} U_{|1} S_{a|1} T_{a|1} + N_a e^{-p_1 M_a} U_{|1} S_{a|1}(1 - T_{a|1}) d_{a|1} \\
&= N_a e^{-p_1 M_a} U_{|1} S_{a|1} [T_{a|1} + (1 - T_{a|1}) d_{a|1}] \\
TM^n_{a|f=2} &= \left(N_a e^{-p_1 M_a} - TM^n_{a|1}\right) U_2 S_{a|2} [T_{a|2} + (1 - T_{a|2}) d_{a|2}] e^{-(p_2-p_1) M_a} \\
&= N_a e^{-p_2 M_a} U_2 S_{a|2} [T_{a|2} + (1 - T_{a|2}) d_{a|2}] \Big[1 - U_1 S_{a|1}[T_{a|1} + (1 - T_{a|1}) d_{a|1}]\Big] \\
TM^n_{a|f=3} &= \Big[\left(N_a e^{-p_1 M_a} - TM^n_{a|1}\right) e^{-(p_2-p_1)} - TM^n_{a|2}\Big] U_3 S_{a|3}[T_{a|3} + (1 - T_{a|3}) d_{a|3}] e^{-(p_3-p_2) M_a} \\
&= N_a e^{-p_3 M_a} U_3 S_{a|3}[T_{a|3} + (1 - T_{a|3}) d_{a|3}] \prod_{i=1}^{2} \{1 - U_i S_{a|i}[T_{a|i} + (1 - T_{a|i}) d_{a|i}]\}
\end{aligned}
$$

Generally,

$$TM_{a|f}^n = N_a e^{-p_f M_a} U_f S_{a|f} \left[T_{a|f} + (1 - T_{a|f}) d_{a|f} \right] \times$$
$$\prod_{i \in p_j < p_f} \left\{ 1 - U_i S_{a|i} \left[T_{a|i} + (1 - T_{a|i}) d_{a|i} \right] \right\}$$

where j is over all fleets. In essence, the total mortality is determined from the numbers-at-age that survived naturally to that point and survived the probability of fishing mortality (retained or discarded and died) from all fleets up to that point in the time-step.

Appendix III
Primary objectives defined by the Commission for the MSE

Table I.1: Primary objectives, evaluated over a simulated ten-year period, accepted by the Commission at the 7th Special Session of the Commission (SS07). Objective 1.1 is a biological sustainability (conservation) objective and objectives 2.1, 2.2, and 2.3 are fishery objectives. Priority objectives are shown in bold text.

GENERAL OBJECTIVE	MEASURABLE OBJECTIVE	MEASURABLE OUTCOME	TIME-FRAME	TOLERANCE	PERFORMANCE METRIC
1.1. KEEP FEMALE SPAWNING BIOMASS ABOVE A LIMIT TO AVOID CRITICAL STOCK SIZES AND CONSERVE SPATIAL POPULATION STRUCTURE	**Maintain the long-term coastwide female spawning stock biomass above a biomass limit reference point (B$_{20\%}$) at least 95% of the time**	$B <$ Spawning Biomass Limit (B_{Lim}) B_{Lim}=20% unfished spawning biomass	Long-term	0.05	$P(SB < SB_{Lim})$ Fail if greater than 0.05
	Maintain a defined minimum proportion of female spawning biomass in each Biological Region	$p_{SB,2} > 5\%$ $p_{SB,3} > 33\%$ $p_{SB,4} > 10\%$ $p_{SB,4B} > 2\%$	Long-term	0.05	$P(p_{SB,R} < p_{SB,R,min})$
2.1 MAINTAIN SPAWNING BIOMASS AT OR ABOVE A LEVEL THAT OPTIMIZES FISHING ACTIVITIES	**Maintain the long-term coastwide female spawning stock biomass at or above a biomass reference point (B$_{36\%}$) 50% or more of the time**	$B <$Spawning Biomass Reference (B_{Thresh}) B_{Thresh}=B$_{36\%}$ unfished spawning biomass	Long-term	0.50	$P(SB < SB_{Targ})$ Fail if greater than 0.5
2.2. PROVIDE DIRECTED FISHING YIELD	**Optimize average coastwide TCEY**	Median coastwide TCEY	Short-term		$Median \ \overline{TCEY}$
	Optimize TCEY among Regulatory Areas	Median TCEY$_A$	Short-term		$Median \ \overline{TCEY_A}$
	Optimize the percentage of the coastwide TCEY among Regulatory Areas	Median %TCEY$_A$	Short-term		$Median \ \overline{\left(\frac{TCEY_A}{TCEY}\right)}$
	Maintain a minimum TCEY for each Regulatory Area	Minimum TCEY$_A$	Short-term		$Median \ Min(TCEY)$
	Maintain a percentage of the coastwide TCEY for each Regulatory Area	Minimum %TCEY$_A$	Short-term		$Median \ Min(\%TCEY)$
2.3. LIMIT VARIABILITY IN MORTALITY LIMITS	**Limit annual changes in the coastwide TCEY**	Annual Change (AC) > 15% in any 3 years	Short-term		$P(AC_3 > 15\%)$
		Median coastwide Average Annual Variability (AAV)	Short-term		$Median \ AAV$
	Limit annual changes in the Regulatory Area TCEY	Annual Change (AC) > 15% in any 3 years	Short-term		$P(AC_3 > 15\%)$
		Average AAV by Regulatory Area (AAV$_A$)	Short-term		$Median \ AAV_A$